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510(k) Summary
BioFire Diagnostics, LLC

FilmArray Gastrointestinal (GI) Panel Kit

Introduction: According to the requirements of 21 CFR 807.92, the following information provides sufficient detail to understand the basis for a determination of substantial equivalence.

Submitted by:

BioFire Diagnostics, LLC
390 Wakara Way
Salt Lake City, UT 84108

Telephone: 801-736-6354
Facsimile: 801-588-0507

Contact: Beth Lingenfelter, ext. 407

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Device Name and Classification:

Trade Name: FilmArray GI Panel

Regulation Number: 21 CFR 866.3990

Classification Name: Gastrointestinal microorganism multiplex nucleic acid-based assay

Predicate Device:

K121454 – Luminex xTAG® Gastrointestinal Pathogen Panel (GPP)

Intended Use:

The FilmArray Gastrointestinal (GI) Panel is a qualitative multiplexed nucleic acid-based *in vitro* diagnostic test intended for use with the FilmArray Instrument. The FilmArray GI Panel is capable of the simultaneous detection and identification of nucleic acids from multiple bacteria, viruses, and parasites directly from stool samples in Cary Blair transport media obtained from individuals with signs and/or symptoms of gastrointestinal infection. The following bacteria (including several diarrheagenic *E. coli/Shigella* pathotypes), parasites, and viruses are identified using the FilmArray GI Panel:

- *Campylobacter* (*C. jejuni/C. coli/C. upsaliensis*)
- *Clostridium difficile* (*C. difficile*) toxin A/B
- *Plesiomonas shigelloides*
- *Salmonella*

- *Vibrio* (*V. parahaemolyticus/V. vulnificus/V. cholerae*) including specific identification of *Vibrio cholerae*
- *Yersinia enterocolitica*
- Enteroaggregative *Escherichia coli* (EAEC)
- Enteropathogenic *Escherichia coli* (EPEC)
- Enterotoxigenic *Escherichia coli* (ETEC) *lt/st*
- Shiga-like toxin-producing *Escherichia coli* (STEC) *stx1/stx2* (including specific identification of the *E. coli* O157 serogroup within STEC)
- *Shigella*/Enteroinvasive *Escherichia coli* (EIEC)
- *Cryptosporidium*
- *Cyclospora cayetanensis*
- *Entamoeba histolytica*
- *Giardia lamblia* (also known as *G. intestinalis* and *G. duodenalis*)
- Adenovirus F 40/41
- Astrovirus
- Norovirus GI/GII
- Rotavirus A
- Sapovirus (Genogroups I, II, IV, and V)

The FilmArray GI Panel is indicated as an aid in the diagnosis of specific agents of gastrointestinal illness and results are meant to be used in conjunction with other clinical, laboratory, and epidemiological data. Positive results do not rule out co-infection with organisms not included in the FilmArray GI Panel. The agent detected may not be the definite cause of the disease.

Concomitant culture is necessary for organism recovery and further typing of bacterial agents.

This device is not intended to monitor or guide treatment for *C. difficile* infection.

Due to the small number of positive specimens collected for certain organisms during the prospective clinical study, performance characteristics for *E. coli* O157, *Plesiomonas shigelloides*, *Yersinia enterocolitica*, Astrovirus, and Rotavirus A were established primarily with retrospective clinical specimens.

Performance characteristics for *Entamoeba histolytica*, and *Vibrio (V. parahaemolyticus, V. vulnificus*, and *Vibrio cholerae)* were established primarily using contrived clinical specimens.

Negative FilmArray GI Panel results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens that are not detected by this test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease.

A gastrointestinal microorganism multiplex nucleic acid-based assay also aids in the detection and identification of acute gastroenteritis in the context of outbreaks.

Device Description:

The FilmArray Gastrointestinal (GI) Panel is a multiplex nucleic acid test designed to be used with the FilmArray Instrument. The FilmArray GI pouch contains freeze-dried reagents to perform nucleic acid purification and nested, multiplex PCR with DNA melt analysis. The FilmArray Gastrointestinal (GI) Panel simultaneously conducts 22 tests for the identification of GI pathogens from stool specimens collected in Cary Blair transport medium (Table 1). Results from the FilmArray GI Panel test are available within about one hour.

Table 1. Bacteria, Viruses, Diarrheagenic *E. coli/Shigella*, and Parasites Detected by the FilmArray GI Panel

Bacteria	**Viruses**
Campylobacter (*C. jejuni/C. coli/C. upsaliensis*) *Clostridium difficile* (toxin A/B) *Plesiomonas shigelloides* *Salmonella* *Vibrio(V. parahaemolyticus/V. vulnificus/V. cholerae)* *Vibrio cholerae* *Yersinia enterocolitica*	Adenovirus F 40/41 Astrovirus Norovirus GI/GII Rotavirus A Sapovirus (Genogroups I, II, IV, and V)
Diarrheagenic *E. coli/Shigella*	**Parasites**
Enteroaggregative *E. coli* (EAEC) Enteropathogenic *E. coli* (EPEC) Enterotoxigenic *E. coli* (ETEC) *lt/st* Shiga toxin-producing *E. coli* (STEC) *stx1/stx2* *E. coli* O157 *Shigella*/Enteroinvasive *E. coli* (EIEC)	*Cryptosporidium* *Cyclospora cayetanensis* *Entamoeba histolytica* *Giardia lamblia*

A test is initiated by loading Hydration Solution into one port of the FilmArray pouch and a stool sample (in Cary Blair transport medium) mixed with the provided Sample Buffer into the other port of the FilmArray GI pouch and placing it in the FilmArray Instrument. The pouch contains all of the reagents required for specimen testing and analysis in a freeze-dried format; the addition of Hydration Solution and Sample/Buffer Mix rehydrates the reagents. After the pouch is prepared, the FilmArray Software guides the user though the steps of placing the pouch into the instrument, scanning the pouch barcode, entering the sample identification, and initiating the run.

The FilmArray Instrument contains a coordinated system of inflatable bladders and seal points, which act on the pouch to control the movement of liquid between the pouch blisters. When a bladder is inflated over a reagent blister, it forces liquid from the blister into connecting channels. Alternatively, when a seal is placed over a connecting channel it acts as a valve to open or close a channel. In addition, electronically controlled pneumatic pistons are positioned over multiple plungers in order to deliver the rehydrated reagents into the blisters at the appropriate

times. Two Peltier devices control heating and cooling of the pouch to drive the PCR reactions and the melt curve analysis.

Nucleic acid extraction occurs within the FilmArray pouch using mechanical and chemical lysis followed by purification using standard magnetic bead technology. After extracting and purifying nucleic acids from the unprocessed sample, the FilmArray performs a nested multiplex PCR that is executed in two stages. During the first stage, the FilmArray performs a single, large volume, highly multiplexed reverse transcription PCR (rt-PCR) reaction. The products from first stage PCR are then diluted and combined with a fresh, primer-free master mix and a fluorescent double stranded DNA binding dye (LC Green® Plus, BioFire). The solution is then distributed to each well of the array. Array wells contain sets of primers designed specifically to amplify sequences internal to the PCR products generated during the first stage PCR reaction. The 2nd stage PCR, or nested PCR, is performed in singleplex fashion in each well of the array. At the conclusion of the 2nd stage PCR, the array is interrogated by melt curve analysis for the detection of signature amplicons denoting the presence of specific targets. A digital camera placed in front of the 2nd stage PCR captures fluorescent images of the PCR reactions and software interprets the data.

The FilmArray Software automatically interprets the results of each DNA melt curve analysis and combines the data with the results of the internal pouch controls to provide a test result for each organism on the panel.

Substantial Equivalence:

The Luminex xTAG® Gastrointestinal Pathogen Panel (GPP) is a qualitative, multiplexed *in vitro* diagnostic assay intended to simultaneously detect and identify microorganism nucleic acids from human stool samples. Testing is performed on pre-treated human stool samples. Table 2 outlines the similarities between the two systems and Table 3 outlines the differences.

Table 2. Similarities Between the FilmArray GI Panel and the Luminex xTAG® Gastrointestinal Pathogen Panel (GPP).

Element	FilmArray GI Panel	Luminex xTAG® Gastrointestinal Pathogen Panel (GPP)
Organisms Detected	*Campylobacter*, toxigenic *Clostridium difficile*, *Salmonella*, Norovirus GI/GII, Rotavirus A, *Cryptosporidium*, *Giardia lamblia*, *E. coli* O157, Shiga toxin-producing *E. coli* (STEC), Enterotoxigenic *E. coli* (ETEC), and *Shigella*/Enteroinvasive *E. coli* (EIEC).	Same See below for differences
Analyte	DNA/RNA	Same
Technological Principles	Multiplex nucleic acid	Same See below for differences

Table 3. Differences Between the FilmArray GI Panel Test System and the Luminex xTAG® Gastrointestinal Pathogen Panel (GPP).

Element	FilmArray GI Panel	Luminex xTAG® Gastrointestinal Pathogen Panel (GPP)
Specimen Types	Human stool sample collected in Cary Blair transport media.	Pre-treated human stool sample.
Organisms Detected	Detects the following *Campylobacter* species: *C. jejuni/C. coli/C. upsaliensis*. Also detects additional *Cryptosporidium* species, *Plesiomonas shigelloides*, *Vibrio* (*V. parahaemolyticus/V. vulnificus/V. cholerae*), *V. cholerae*, *Yersinia enterocolitica*, Adenovirus F40/41, Astrovirus, Sapovirus (Genogroups I, II, IV, and V), *Cyclospora cayetanensis*, *Entamoeba histolytica*, Enteropathogenic *E. coli* (EPEC), Enteroinvasive *E. coli* (EIEC), and Enteroaggregative *E. coli* (EAEC).	Detects the following *Campylobacter* species: *C. jejuni*, *C. coli*, and *C. lari*. Only detects the following *Cryptosporidium* species: *C. parvum* and *C. hominis*.
Technological Principles	Nested multiplex RT-PCR followed by high resolution melting analysis to confirm identity of amplified product.	Multiplex RT-PCR and multiplex TSPE followed by Fluorescence-activated sorting of labeled beads coupled to streptavidin-conjugated biotinylated products.
Instrumentation	FilmArray Instrument	Nucleic Acid Purification System PCR Thermocycler Luminex® 100/200™ or MAGPIX instruments
Time to result	Less than 1 hour	Approximately 5 hours
Reagent Storage	Room temperature	Reagents stored at 4°C and -20°C.
Sample Preparation Method	Sample Processing is automated in the FilmArray Instrument.	Up front sample processing is required to extract nucleic acid.
Test Interpretation	Automated test interpretation and report generation. User cannot access raw data.	Semi-automated test interpretation. User must review all "no call" results to determine cause and retesting strategy.
Controls	Two controls are included in each reagent pouch to control for sample processing and both stages of PCR and melt analysis.	Internal control added to each sample. External control processed with each batch of samples.

Summary of Performance Data

Clinical Performance

The clinical performance of the FilmArray GI Panel was established during a multi-center study conducted at four geographically distinct U.S. study sites (Pacific, North Central, Great Lakes, and Northeast regions) between May and September, 2013. A total of 1578 prospective residual stool specimens in Cary Blair transport media were acquired for the clinical study; 22 of these were excluded. The most common reasons for exclusion were that a valid external control was not completed on the day of testing, that the specimen was not plated to all of the appropriate bacterial culture media required for the reference method, or that the specimen was beyond four days from the date of collection. The final data set consisted of 1556 specimens. Table 4 provides a summary of demographic information for the 1556 specimens included in the prospective study.

Table 4. Demographic Summary for Prospective FilmArray GI Panel Clinical Evaluation

Prospective Study Specimens	
Total Specimens	1556
Sex	**Number of Specimens (%)**
Male	718 (46%)
Female	838 (54%)
Age Group	**Number of Specimens (%)**
<1 year	121 (8%)
1-5 years	418 (27%)
6-12 years	193 (12%)
13-21 years	240 (15%)
22-64 years	411 (26%)
65+ years	173 (11%)
Status	**Number of Specimens (%)**
Outpatient	1350 (87%)
Hospitalized	164 (11%)
Emergency	42 (3%)

The performance of the FilmArray GI Panel was evaluated by comparing the FilmArray GI Panel test result for each member of the panel with the appropriate comparator/reference methods shown in the table below.

Table 5. Comparator Methods for FilmArray GI Panel Clinical Evaluation

FilmArray Test Results	Reference/Comparator Method
Campylobacter	Stool culture[b] (Blood agar, Blood agar with Ampicillin, MacConkey agar, Sorbitol-MacConkey agar, GN broth + Hektoen enteric agar, Campylobacter agar, Cefsulodin-Irgasan™-Novobiocin agar, and Thiosulfate Citrate Bile Salts agar) with standard manual and automated microbiological/biochemical identification methods
E. coli O157[a]	
Plesiomonas shigelloides	
Salmonella	
Vibrio and *V. cholerae*	
Yersinia enterocolitica	
STEC (*stx1/2*)	PCR with Bi-directional Sequencing[h]
ETEC	
EPEC[c]	
EIEC/*Shigella*[d]	
EAEC	
Adenovirus F 40/41	
Astrovirus	
Norovirus GI/GII[e]	
Rotavirus A	
Sapovirus[f]	
Clostridium difficile toxin A/B	
Cryptosporidium	
Giardia lamblia[g]	
Cyclospora cayetanensis	
Entamoeba histolytica	

[a] The *E. coli* O157 comparator method data were only used to determine the accuracy of the FilmArray determination of *E. coli* O157 detected or not detected for specimens in which FilmArray detected STEC.
[b] Any bacteria isolated from stool culture that could not be identified to the species level by laboratory methods were sequenced using an assay capable of providing species information (e.g., 16S).
[c] A result for EPEC is only reported in the absence of STEC (same algorithm as FilmArray).
[d] *Shigella* may be identified by routine culture methods; however, culture detection will be reported for informational purposes only.
[e] CDC Calicinet assays (non-sequenceable) were used for the comparator method for Norovirus.
[f] Sapovirus comparator assays consisted of one well-validated, sequenceable assay and one published assay that was not sequenceable.
[g] *G. lamblia* comparator assays consisted of one well-validated, sequenceable assay and one published assay that was not sequenceable.
[h] PCR assays were designed to amplify different sequences than those targeted by FilmArray GI. Positive results for sequenceable assays required a sequencing result of adequate quality to match a sequence of the expected organism/gene deposited in the National Center for Biotechnology Information (NCBI) GenBank database (www.ncbi.nlm.nih.gov), with an acceptable E-value.

A total of 1556 specimens were evaluated in this study. Of these specimens, 832 (53.5%) were positive for at least one analyte. Clinical sensitivity or positive percent agreement (PPA) was calculated as 100% x (TP / (TP + FN)). True positive (TP) indicates that both the FilmArray GI Panel and reference/comparator method had a positive result for this specific analyte, and false negative (FN) indicates that the FilmArray result was negative while the comparator result was positive. Specificity or negative percent agreement (NPA) was calculated as 100% x (TN / (TN + FP)). True negative (TN) indicates that both the FilmArray GI Panel and the

reference/comparator method had negative results, and a false positive (FP) indicates that the FilmArray GI Panel result was positive but the comparator result was negative. The exact binomial two-sided 95% confidence interval was calculated. The results are summarized in Table 6.

Table 6. FilmArray GI Clinical Performance Summary

Bacteria	Sensitivity/PPA[a]			Specificity/NPA[a]		
	TP/(TP + FN)	%	95% CI	TN/(TN + FP)	%	95% CI
Campylobacter (*C. jejuni/C. coli/C. upsaliensis*)	34/35[b]	97.1	85.1-99.9	1497/1521[b]	98.4	97.7-99.0
Clostridium difficile toxin A/B[a]	163/165[c]	98.8	95.7-99.9	1350/1391[c]	97.1	96.0-97.9
Plesiomonas shigelloides	3/3	100	29.2-100	1538/1553[d]	99.0	98.4-99.5
Salmonella	31/31	100	88.8-100	1519/1525[e]	99.6	99.1-99.9
Vibrio (*V. parahaemolyticus/V. vulnificus/V. cholerae*)	0/0	-	-	1554/1556[f]	99.9	99.5-100
Vibrio cholerae	0/0	-	-	1555/1556[g]	99.9	99.6-100
Yersinia enterocolitica	1/1	100	N/A	1555/1555	100	99.8-100
Diarrheagenic *E. coli/Shigella*	**Positive Percent Agreement (PPA)[a]**			**Negative Percent Agreement (NPA)[a]**		
	TP/(TP + FN)	**%**	**95% CI**	**TN/(TN + FP)**	**%**	**95% CI**
Enteroaqggregative *E. coli* (EAEC)	82/83	98.8	93.5-100	1446/1473[h]	98.2	97.3-98.8
Enteropathogenic *E.* coli (EPEC)	314/317	99.1	97.3-99.8	1167/1201[i]	97.2	96.1-98.0
Enterotoxigenic *E. coli* (ETEC) *lt/st*	22/22	100	84.6-100	1525/1534[j]	99.4	98.9-99.7
Shiga-like toxin-producing *E. coli* (STEC) *stx1/stx2*	33/33	100	89.4-100	1518/1523[k]	99.7	99.2-99.9
E. coli O157[a]	3/3	100	29.2-100	34/35[l]	97.1	85.1-99.9
Shigella/Enteroinvasive *E. coli* (EIEC)	47/49	95.9	86.0-99.5	1505/1507	99.9	99.5-100
Parasites	**Positive Percent Agreement (PPA)[a]**			**Negative Percent Agreement (NPA)[a]**		
	TP/(TP + FN)	**%**	**95% CI**	**TN/(TN + FP)**	**%**	**95% CI**
Cryptosporidium	18/18	100	81.5-100	1532/1538[m]	99.6	99.2-99.9
Cyclospora cayetanensis	19/19	100	82.4-100	1537/1537	100	99.8-100
Entamoeba histolytica	0/0	-	-	1556/1556	100	99.8-100
Giardia lamblia	20/20	100	83.2-100	1529/1536[n]	99.5	99.1-99.8
Viruses	**Positive Percent Agreement (PPA)[a]**			**Negative Percent Agreement (NPA)[a]**		
	TP/(TP + FN)	**%**	**95% CI**	**TN/(TN + FP)**	**%**	**95% CI**
Adenovirus F 40/41	42/44[o]	95.5	84.5-99.4	1499/1512[o]	99.1	98.5-99.5
Astrovirus	7/7	100	59.0-100	1548/1549[p]	99.9	99.6-100
Norovirus GI/GII	52/55[q]	94.5	84.9-98.9	1483/1501[q]	98.8	98.1-99.3
Rotavirus A	6/6	100	54.1-100	1538/1550[r]	99.2	98.7-99.6
Sapovirus (Genogroups I, II, IV, and V)	46/46	100	92.3-100	1497/1510[s]	99.1	98.5-99.5

[a] *C. difficile* performance is reported as positive percent agreement and negative percent agreement, and *E. coli* O157 performance is reported as sensitivity/specificity, in contrast to the headings of their respective sections. The performance measures of sensitivity and specificity only refer to those analytes for which the gold-standard bacterial culture was used as the reference method: *Campylobacter*, *E. coli* O157, *Plesiomonas shigelloides*, *Salmonella*, *Vibrio*, *Vibrio cholerae*, and *Yersinia*

enterocolitica. Performance measures of positive percent agreement (PPA) and negative percent agreement (NPA) refer to all other analytes, for which PCR/sequencing assays were used as comparator methods.
[b] *Campylobacter jejuni* subsp. *doylei* was identified in the single false negative specimen using bi-directional sequence analysis. *Campylobacter* was detected in 19/24 false positive specimens using bi-directional sequence analysis.
[c] *C. difficile* was detected in 1/2 false negative specimens and 41/41 false positive specimens using bi-directional sequence analysis.
[d] *P. shigelloides* was detected in 15/15 false positive specimens using bi-directional sequence analysis.
[e] *Salmonella* was detected in 6/6 false positive specimens using bi-directional sequence analysis.
[f] *Vibrio* was detected in 2/2 false positive specimens using bi-directional sequence analysis.
[g] *V. cholerae* was detected in the single false positive specimen using bi-directional sequence analysis.
[h] EAEC was detected in 27/27 false positive specimens using bi-directional sequence analysis.
[i] EPEC was detected in 23/34 false positive specimens using bi-directional sequence analysis.
[j] ETEC was detected in 6/9 false positive specimens using bi-directional sequence analysis. The three remaining false positive results were determined to have been caused by cross-reactivity with *Citrobacter koseri* (2 instances), and *Hafnia alvei* (1 instance). These bacteria contain a variant of the *fliP* gene with sequence similarity to assay primers.
[k] STEC was detected in 5/5 false positive specimens using bi-directional sequence analysis.
[l] *E. coli* O157 was detected in the single false positive specimen using bi-directional sequence analysis.
[m] *Cryptosporidium* was detected in 6/6 false positive specimens using bi-directional sequence analysis.
[n] *G. lamblia* was detected in 4/7 false positive specimens using bi-directional sequence analysis. Two false positive results appear to be caused by cross-reactivity with *Bifidobacterium longum* and *Ruminococcus callidus*.
[o] Adenovirus was detected in 1/2 false negative specimens and 11/13 false positive specimens using bi-directional sequence analysis
[p] Astrovirus was detected in the single false positive specimen using bi-directional sequence analysis.
[q] The FilmArray GI system detected Norovirus in 1/3 false negative specimens when retested. Norovirus was detected in 1/2 remaining false negative specimens and 8/18 false positive specimens using bi-directional sequence analysis.
[r] Rotavirus A was detected in 11/12 false positive specimens using bi-directional sequence analysis.
[s] Sapovirus was detected in 12/13 false positive specimens using bi-directional sequence analysis.

FilmArray GI reports genus level (or multiple species group) results for three bacterial analytes; i.e., *Campylobacter* (*C. jejuni/C. coli/C. upsaliensis*), *Salmonella*, and *Vibrio* (*V. parahaemolyticus/V. vulnificus/V. cholerae*). Standard laboratory methods identified various species/serovars within each of these groups during the clinical evaluation. Where standard methods did not provide a species identification, bi-directional sequencing was used to identify the species of the isolate. Stratification of performance by species/serovar is presented below. For *Vibrio*, no organisms were isolated by the culture methods; however, bi-directional sequencing from the original specimens identified one *V. parahaemolyticus* and one *V. cholerae*.

Table 7. *Campylobacter* Clinical Performance Stratified by Species

***Campylobacter* species**[a]	**Sensitivity**
C. jejuni[b]	31/31 (100%)
C. coli	2/2 (100%)
C. jejuni subsp. *doylei*	0/1 (0%)
C. upsaliensis	1/1 (100%)
Overall *Campylobacter*	**34/35 (97.1%) 95%CI = 81.3-99.3%**

[a] Fifteen (15) *Campylobacter* were not speciated by the source laboratory and were subject to sequencing of the *cadF* gene. This method identified 11 *C. jejuni*, two *C. coli*, one *C. jejuni* subsp. *doylei*, and one *C. upsaliensis*.
[b] Two *C. jejuni* were originally identified by the source lab as "*Campylobacter* species". Sequencing of the isolates provided by the laboratory identified them as *C. jejuni*. However, molecular testing of the specimen from which the isolates were obtained also detected the presence of *C. upsaliensis*, representing co-infection by these two species.

Table 8. *Salmonella* Clinical Performance Stratified by Species/Serovar

***Salmonella* species/serovar**	**Sensitivity**
S. enterica ser. Enteritidis	7/7 (100%)
S. enterica ser. Typhimurium (i:-)	7/7 (100%)
S. enterica ser. Typhimurium	3/3 (100%)
S. enterica ser. Javiana	2/2 (100%)
S. enterica ser. Newport	2/2 (100%)
S. enterica ser. Agbeni	1/1 (100%)
S. enterica ser. Berta	1/1 (100%)
S. enterica ser. Ealing	1/1 (100%)
S. enterica ser. Gaminara	1/1 (100%)
S. enterica ser. Infantis	1/1 (100%)
S. enterica ser. Mbandaka	1/1 (100%)
S. enterica ser. Miami	1/1 (100%)
S. enterica ser. Muenchen	1/1 (100%)
S. enterica ser. Paratyphi B var L-Tartrate	1/1 (100%)
S. enterica ser. Thompson	1/1 (100%)
Overall *Salmonella*	**31/31 (100%)** **95%CI = 88.8-100%**

The FilmArray GI Panel reported multiple organism detections (i.e., mixed infections) for a total of 262 specimens. This represents 31.5% of positive specimens (262/832) and 16.8% of all specimens (262/1556). The majority of multiple detections (199/262; 76.0%) contained two organisms, while 19.1% (50/262) contained three organisms, 3.4% (9/262) contained four organisms, 1.1% (3/262) contained five organisms, and 0.4% (1/262) contained six organisms. The three organisms that were most prevalent in co-infections were also the three most prevalent organisms in the study as a whole (i.e., EPEC, *C. difficile*, and EAEC). Out of the 262 specimens with multiple detections, 144 specimens (55.0%; 144/262) were concordant with the reference methods. One hundred eighteen specimens (45.0%; 118/262) contained one or more organisms that had not been detected by the reference/comparator methods (i.e., 139 false positive results); however, bi-directional sequence analysis confirmed the presence of the analyte for 88.5% (123/139) of the discrepant results.

Table 9. Prevalence of Analytes in Mixed Infections as determined by the FilmArray GI Panel

Analyte	Prevalence in Mixed Infections *N* = 262	
	No.	%
Bacteria		
Campylobacter	30	11.5%
Clostridium difficile toxin A/B	109	41.6%
Plesiomonas shigelloides	16	6.1%
Salmonella	15	5.7%
Vibrio	1	0.4%
Vibrio cholerae	1	0.4%
Yersinia enterocolitica	1	0.4%
Diarrheagenic *E. coli/Shigella*		
Enteroaggregative *E. coli* (EAEC)	67	25.6%
Enteropathogenic *E. coli* (EPEC)	159	60.7%
Enterotoxigenic *E. coli* (ETEC) *lt/st*	26	9.9%
Shiga-like toxin-producing *E. coli* (STEC) *stx1/stx2*	13	5.0%
E. coli O157	1	0.4%
Shigella / Enteroinvasive *E. coli* (EIEC)	17	6.5%
Parasites		
Cryptosporidium	11	4.2%
Cyclospora cayetanensis	2	0.8%
Entamoeba histolytica	0	0%
Giardia lamblia	14	5.3%
Viruses		
Adenovirus F 40/41	34	13.0%
Astrovirus	4	1.5%
Norovirus GI/GII	43	16.4%
Rotavirus A	10	3.8%
Sapovirus	33	12.6%

The most prevalent mixed infection was *C. difficile* with EPEC (2.0% of all specimens; 32/1556) followed by EAEC with EPEC (1% of all specimens; 15/1556); as previously stated these were the most prevalent organisms detected in the study. Mixed infections were observed for all combinations of analyte classes (e.g. bacteria with viruses, diarrheagenic *E. coli/Shigella* with parasites) and co-infections were observed within classes (e.g. three diarrheagenic *E. coli/Shigella* combined; ETEC, EAEC, and STEC).

Table 10. Most Prevalent Multiple Detection Combinations (≥5 instances) as Determined by the FilmArray GI Panel

Multiple Detection Combination	Number of Specimens
C. difficile toxin A/B + EPEC	32
EAEC + EPEC	15
Campylobacter + EPEC	11
EPEC + Sapovirus	10
Adenovirus + EPEC	9
EPEC + Norovirus GI/GII	9
C. difficile toxin A/B + EAEC	7
C. difficile toxin A/B + Norovirus GI/GII	6
C. difficile toxin A/B + STEC *stx1/stx2*	5
EPEC + ETEC *lt/st*	5
EPEC + *G. lamblia*	5
EPEC + *Shigella/EIEC*	5

The overall success rate for initial specimen tests in the prospective study was 99.4% (1544/1557). Four tests were incomplete due to software errors (3) or a user aborted run (1), and nine tests were invalid due to pouch control failures. All specimens but one were retested within four days of specimen collection and were successful after a single retest, for a final success rate of 99.9% (1556/1557).

Testing of Preselected Archived Specimens

Several analytes were either not encountered or had a low prevalence in the clinical study. To supplement the results of the prospective clinical study, an evaluation of 222 preselected archived specimens was performed. These specimens were archived clinical specimens that were selected because they had previously tested positive for one of the following analytes: *E. coli* O157, *P. shigelloides*, *Y. enterocolitica*, *Vibrio*, Astrovirus, Rotavirus, and *E. histolytica*, or had been negative in previous laboratory testing. Prior to testing with the FilmArray GI Panel, the presence (or absence for negative specimens) of the expected analytes was verified in each specimen using analyte-specific PCR followed by bi-directional sequencing.

The specimens were organized into "test panels" and randomized such that the users performing the FilmArray GI Panel testing were blinded as to the expected test result. A summary of the available demographic information of the tested samples is provided in Table 11 and the results of the FilmArray GI testing are presented in Table 12.

Table 11. Demographic Summary for Preselected Archived Specimens

Preselected Archived Specimens	
Total Specimens	222
Sex	**Number of Specimens (%)**
Male	57 (25.7%)
Female	48 (21.6%)
Unknown	117 (52.7%)
Age Group	**Number of Specimens (%)**
<1 year	12 (5.4%)
1-5 years	36 (16.2%)
6-12 years	15 (6.8%)
13-21 years	11 (5%)
22-64 years	18 (8.1%)
65+ years	4 (1.8%)
Unknown	126 (56.8%)

Table 12. FilmArray GI Panel Archived Specimen Performance Data Summary

Analyte	Positive Percent Agreement (PPA)			Negative Percent Agreement (NPA)		
	TP/(TP + FN)	%	95% CI	TN/(TN + FP)	%	95% CI
Bacteria						
Plesiomonas shigelloides	12/12	100	73.5-100	107/107	100	96.6-100
Vibrio	1/1	100	N/A	127/127	100	97.1-100
Yersinia enterocolitica	8/8	100	63.1-100	117/117	100	96.9-100
Diarrheagenic *E. coli/Shigella*						
(STEC) *E. coli* O157[a]	19/19	100	82.4-100	0/0	-	-
Parasites						
Cryptosporidium	29/30	96.7	82.8-99.9	66/66	100	94.6-100
Entamoeba histolytica	2/2	100	15.8-100	123/123	100	97.0-100
Giardia lamblia	26/26	100	86.8-100	66/66	100	94.6-100
Viruses						
Astrovirus	31/32	96.9	83.8-99.9	91/91	100	96.0-100
Rotavirus A	29/29	100	88.1-100	65/65	100	94.5-100

[a] No non-O157 STEC were included in the data set; therefore, negative percent agreement (NPA) could not be calculated for *E. coli* O157.

Testing of Contrived Specimens

Several analytes, such as *Entamoeba histolytica*, are so rare that both prospective and archived testing efforts were insufficient to demonstrate system performance. To supplement the prospective and archived data, an evaluation of contrived specimens was performed. Surrogate clinical specimens were prepared using residual specimens from the prospective clinical study that had previously tested negative for all GI panel analytes by FilmArray GI and comparator methods. Specimens were spiked at clinically relevant levels using five different quantified

strains for each organism (or unspiked; at least 50 of each). The analyte status of each contrived specimen was blinded to the users analyzing the specimens, and the specimens were randomized before testing. The results of the FilmArray GI testing are presented in the table below:

Table 13. FilmArray GI Panel Performance using Contrived Specimens

Analyte	Positive Percent Agreement (PPA)			Negative Percent Agreement (NPA)		
	TP/(TP + FN)	%	95% CI	TN/(TN + FP)	%	95% CI
Entamoeba histolytica	44/50	88.0	75.7-95.5	75/75	100	95.2-100
Plesiomonas shigelloides	70/70	100	94.9-100	105/105	100	96.5-100
Vibrio[a]	112/115	97.4	92.6-99.5	60/60	100	94.0-100
V. cholerae[b]	55/65	84.6	73.5-92.4	110/110	100	96.7-100
Yersinia enterocolitica	65/65	100	94.5-100	110/110	100	96.7-100

[a] Includes 64/65 *V. cholerae* (five different strains were used in spiking; one specimen spiked near the assay limit of detection was not detected) and 48/50 non-*V. cholerae* (four *V. parahaemolyticus* strains and one *V. vulnificus* strain were used in spiking; two specimens spiked with *V. parahaemolyticus* near the assay limit of detection were not detected).
[b] Ten (10) of these specimens were spiked with an isolate which was found to have a highly divergent *toxR* gene that was not present in the NCBI database and non-reactive with the FilmArray GI Panel *V. cholerae* assay. The FilmArray GI Panel *Vibrio* assay was positive for nine of these specimens.

Selected Analytic Studies

Limit of Detection

A study was performed to determine the analytical sensitivity, or limit of detection (LoD), of the FilmArray GI Panel for each test result included in the panel. LoD (or LoD_{95}) is defined as the lowest concentration of organism that can be consistently detected ($\geq$ 95% of samples test positive) in the defined sample type (stool in Cary Blair transport medium).

The LoD for each organism was estimated with limiting dilutions as single-spiked and multi-spiked samples (up to four organisms per mix), to provide an estimated LoD concentration, and to determine whether assay sensitivity is affected by the presence of multiple panel organisms in a single sample.

Confirmation of LoDs was performed by spiking organism (single or multi-spike) at the LoD estimate determined by the dilutions series, into 20 independent stool samples. LoD was confirmed when the correct organism/assay results were obtained from at least 19 of the 20 samples (19/20 = 95%) tested.

Table 14. Table of Confirmed Limit of Detection (LoD) for GI Panel Analytes

GI Panel Test Result	Species/Isolate Tested	Confirmed LoD Concentration	Detection at LoD Concentration
BACTERIA			
Campylobacter	*Campylobacter coli* ATCC 33559	4×10^4 cells/mL	20/20 100%
	Campylobacter jejuni ATCC BAA-1234		20/20 100%
	Campylobacter upsaliensis ATCC BAA-1059		20/20 100%
Clostridium difficile (toxin A/B)	*Clostridium difficile* Toxinotype 0 A+B+ ATCC 9689	4×10^5 cells/mL	20/20 100%
	Clostridium difficile (NAP1) Toxinotype III A+B+ Zeptometrix #801619	4×10^4 cells/mL	19/20 95%
Plesiomonas shigelloides	*Plesiomonas shigelloides* ATCC 14029	1×10^3 CFU/mL	20/20 100%
Salmonella	*Salmonella bongori* O66:H1z41:H2- SGSC RKS#3041 SarC11	1×10^4 CFU/mL	20/20 100%
	Salmonella enterica ssp. *enterica* Serovar Typhimurium O1,4,[5],12:H1i:H21,2 SGSC RKS#4194 SarC1	5×10^3 CFU/mL	20/20 100%
Vibrio and *Vibrio cholerae*	*Vibrio cholerae* Ogawa serotype O:1 ATCC 14035	8×10^3 cells/mL	20/20 100%
	Vibrio parahaemolyticus ATCC 17802	8×10^4 cells/mL	20/20 100%
Yersinia enterocolitica	*Yersinia enterocolitica* ATCC 9610 Biovar1 serogroup O:8	5×10^4 CFU/mL	20/20 100%
DIARRHEAGENIC *E. coli/Shigella*			
Enteroaggregative *E. coli* (EAEC)	*Escherichia coli* O92:H33 STEC Center # JM221	1×10^4 CFU/mL	20/20 100%
Enteropathogenic *E. coli* (EPEC)	*Escherichia coli* E2348/69 O127:H6 STEC Center	1×10^3 CFU/mL	20/20 100%
Enterotoxigenic *E. coli* (ETEC) *lt/st*	*Escherichia coli* H10407 O78:H11 ATCC 35401	1×10^3 CFU/mL	20/20 100%
Shiga-like toxin-producing *E. coli* (STEC) *stx1/stx2*	*Escherichia coli* O25:H11 ATCC BAA-2196	1×10^3 CFU/mL	20/20 100%
E. coli O157	*Escherichia coli* O157:H7 ATCC 43895	1×10^4 CFU/mL	20/20 100%
Shigella/Enteroinvasive *E. coli* (EIEC)	Escherichia *coli* O29:NM ATCC 43892	5×10^3 CFU/mL	20/20 100%
	Shigella sonnei ATCC 29930	100 CFU/mL	20/20 100%
PARASITES			
Cryptosporidium [a]	*Cryptosporidium parvum* *Iowa* isolate (Harley Moon) Waterborne, Inc. P102C	5×10^3 oocysts/mL	20/20 100%
	Cryptosporidium hominis Clinical Specimen		20/20 100%
Cyclospora cayetanensis	*Cyclospora cayetanensis* Clinical Specimen	180 genome equivalents (GE)/mL	20/20 100%

GI Panel Test Result	Species/Isolate Tested	Confirmed LoD Concentration	Detection at LoD Concentration
Entamoeba histolytica	*Entamoeba histolytica* HM-1:IMSS ATCC 30459	2 x 10^3 cells/mL	19/20 95%
Giardia lamblia	*Giardia intestinalis* (aka *G. lamblia*) ATCC 30957	50 cells/mL	20/20 100%
VIRUSES			
Adenovirus F 40/41	Adenovirus F40 ATCC VR-931	1 $TCID_{50}$/mL	20/20 100%
	Adenovirus F41 ATCC VR-930	100 $TCID_{50}$/mL	20/20 100%
Astrovirus	Astrovirus - Type 8 NCPV#1003071v	50 FFU/mL	20/20 100%
Norovirus GI/GII	Norovirus GI Clinical Specimen	1 x 10^4 RNA copies/mL	19/20 95%
	Norovirus GII Clinical Specimen		20/20 100%
Rotavirus A	Rotavirus A - Type G4 [P6] NCPV#0904053v	1 x 10^5 FFU/mL	20/20 100%
Sapovirus	Sapovirus (Genogroup I) Clinical Specimen	1.1 x 10^7 RNA copies /mL	20/20 100%

[a] Limited testing with a clinical specimen containing *Cryptosporidium meleagridis* indicates that the LoD for this species is similar to that of *C. parvum* and *C. hominis*.

Inclusivity

The analytical reactivity (inclusivity) of the FilmArray GI Panel was evaluated with a collection of 270 isolates that represent the diversity of the FilmArray GI Panel analytes. Isolates were selected to represent relevant subspecies or serotypes and selection was biased toward more common species and known human pathogens. When possible, *in silico* analysis of sequence data was used to make predictions of assay reactivity for less common species, strains, serovars, or serotypes that were not tested.

Organisms were tested at concentrations near the limit of detection (LoD). If a sample containing a particular strain was positive (detected) at the initial test level, no further testing was required. If a strain was not detected, the strain was retested at the same level (up to five additional times) and if necessary, additional testing was performed at 10- and 100-fold higher concentrations to determine if the strain can be detected by the GI Panel. Based upon predicted assay reactivity, a few select isolates were initially tested at a high concentration, followed by evaluation at lower concentrations if detection was observed. Results are provided below for each FilmArray GI Panel test result.

Table 15. FilmArray *Campylobacter* Inclusivity Results (*C. coli/C. jejuni/C. upsaliensis*)

Organism	Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Campylobacter coli[a]	ATCC BAA-1061	1.2 x 10^5	3×LoD
	BEI HM-296	1.2 x 10^5	3×LoD
	ATCC43485	1.2 x 10^5	3×LoD
	ATCC 43478	1.2 x 10^5	3×LoD

Organism	Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
	ATCC 33559[b]	4.0×10^4	1×LoD
Campylobacter jejuni subsp. *doylei*[c]	ATCC 49349	4.0×10^6	Not Detected[c]
	ATCC 49351	4.0×10^6	100×LoD[c]
	ATCC 49350	4.0×10^6	Not Detected[c]
Campylobacter jejuni subsp. *jejuni*	ATCC 43430	1.2×10^5	3×LoD
	ATCC BAA-1062	1.2×10^5	3×LoD
	ATCC BAA-1234[b]	4.0×10^4	1×LoD
	BEI NR-128	1.2×10^5	3×LoD
Campylobacter upsaliensis	ATCC BAA-1059	4.0×10^4	1×LoD
	CCUG 24191	1.2×10^5	3×LoD
	ATCC 43953	1.2×10^5	3×LoD
	ATCC 43954[d]	4.0×10^6	Not Detected[d]
	ATCC 49815	1.2×10^5	3×LoD
	BEI HM-297	1.2×10^5	3×LoD

[a] *In silico* analysis indicates primer mismatches that might lead to reduced assay sensitivity or lack of reactivity with 11/138 *C. coli* sequences.
[b] Isolate was used to establish the LoD for this assay.
[c] *In silico* analysis indicates primer mismatches that might lead to reduced assay sensitivity for this subspecies.
[d] Sequencing under the primers identified an insertion/deletion in the primer binding region of the target gene.

Table 16. FilmArray *Clostridium difficile* toxin A/B Inclusivity Results

Organism	Toxinotype	Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Clostridium difficile	0 A+B+	ATCC 9689[a]	4.0×10^5	1xLoD
		ATCC BAA-1382	1.2×10^6	3×LoD
		ATCC 17857	1.2×10^6	3×LoD
		ATCC 17858	1.2×10^6	3×LoD
		ATCC 43255	1.2×10^6	3×LoD
		ATCC 43594	1.2×10^6	3×LoD
		ATCC 43596	1.2×10^6	3×LoD
		ATCC 43599	1.2×10^6	3×LoD
		ATCC 43600	1.2×10^6	3×LoD
		ATCC 51695	1.2×10^6	3×LoD
		ATCC 700792	1.2×10^6	3×LoD
	III A+B+	ATCC BAA-1805 (NAP1)	1.2×10^6	3×LoD

Organism	Toxinotype	Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
		Zeptometrix #0801619 (NAP1)[a]	4.0×10^4	1×LoD
	V A+B+	ATCC BAA-1875	1.2×10^6	3×LoD
	VIII A-B+	ATCC 43598	1.2×10^6	3×LoD
	X A-B+	CCUG 8864	1.2×10^6	3×LoD
	XII A+B+	ATCC BAA-1812	1.2×10^6	3×LoD
	XXII A+B (unknown)	ATCC BAA-1814	1.2×10^6	3×LoD

[a] This isolate was used to establish the LoD for this assay.

Table 17. FilmArray *Plesiomonas shigelloides* Inclusivity Results

Organism	Geographic Isolation	Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Plesiomonas shigelloides	CDC 3085-55	ATCC 14029[a]	1.0×10^3	1xLoD
	CDC 16408	ATCC 14030	3.0×10^3	3×LoD
	Dakar, Senegal	ATCC 51572	3.0×10^3	3×LoD
	Unknown	ATCC 51903	3.0×10^3	3×LoD
	Colorado	CDPH HUM-2011019465	3.0×10^3	3×LoD
	Czech Republic	NIPH-Czech Republic 6300	3.0×10^3	3×LoD

[a] This isolate was used to establish the LoD for this assay. The organism was quantified in CFU/mL by plate enumeration.

Table 18. FilmArray *Salmonella* Inclusivity Results

Organism (species, subspecies, and serovar)		Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Salmonella bongori		SGSC RKS 3041[a]	1.0×10^4	1xLoD
		NCTC 10946	3.0×10^4	3×LoD
		SGSC RKS 3044	3.0×10^4	3×LoD
Salmonella enterica subsp. *salamae II*		SGSC RKS 2985	1.5×10^4	3×LoD
Salmonella enterica subsp. *arizonae IIIa*		SGSC RKS 2980	1.5×10^4	3×LoD
Salmonella enterica subsp. *diarizonae IIIb*		SGSC RKS 2978	1.5×10^4	3×LoD
Salmonella enterica subsp. *houtenae IV*		SGSC RKS 3027	1.5×10^4	3×LoD
Salmonella enterica subsp. *indica VI*		SGSC RKS 2995	1.5×10^4	3×LoD
Salmonella enterica	Typhimurium	SGSC RKS 4194[a]	5.0×10^3	1xLoD

Organism (species, subspecies, and serovar)		Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
subsp. *enterica*[b]	Enteritidis	ATCC BAA-708	1.5×10^4	3×LoD
	Newport	ATCC 27869	1.5×10^4	3×LoD
	Javiana	ATCC 10721	1.5×10^4	3×LoD
	Heidelberg	ATCC 8326	1.5×10^4	3×LoD
	Montevideo	ATCC BAA-710	1.5×10^4	3×LoD
	I 4,[5],12:i:-	Cornell CU0580	1.5×10^4	3×LoD
	Oranienburg	ATCC 9239	1.5×10^4	3×LoD
	Saintpaul	ATCC 9712	1.5×10^4	3×LoD
	Muenchen	ATCC 8388	1.5×10^4	3×LoD
	Braenderup	ATCC 700136	1.5×10^4	3×LoD
	Infantis	ATCC BAA-1675	1.5×10^4	3×LoD
	Thompson	ATCC 8391	1.5×10^4	3×LoD
	Mississippi	Cornell CU0633	1.5×10^4	3×LoD
	Paratyphi B var. L(+) tartrate+ (formerly java)	CCUG 9561	1.5×10^4	3×LoD
	Typhi (Purified DNA)[b]	ATCC 700931D-5	1.5×10^4	3×LoD
	Agona	ATCC 51957	1.5×10^4	3×LoD
	Schwarzengrund	CCUG 21280	1.5×10^4	3×LoD
	Bareilly	ATCC 9115	1.5×10^4	3×LoD
	Hadar	ATCC 51956	1.5×10^4	3×LoD

[a] This isolate was used to establish the LoD for this assay. The organism was quantified in CFU/mL by plate enumeration.
[b] Purified DNA was quantified in GE/mL by spectrophotometer.

Note: In addition to those evaluated in this study, *in silico* sequence analysis indicates the FilmArray *Salmonella* assay should react with all species and subspecies of *Salmonella*, including all serotypes of S. *enterica* subsp. *enterica.*

Table 19. FilmArray *Vibrio* (*V. parahaemolyticus/V. vulnificus/V. cholerae*) and *Vibrio cholerae* Inclusivity Results

Organism (species, biotype and serotype)		Source/Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Vibrio cholerae	O:1 Ogawa	ATCC 14035[a]	8.0×10^3	1xLoD
	O:1 Inaba, Biotype El Tor	BEI NR-147	2.4×10^4	3xLoD
	O:1 Ogawa, Biotype El Tor	BEI NR-148	2.4×10^4	3xLoD
	non-O:1,non-O:139 (O:2)	BEI NR-149	2.4×10^4	3xLoD

Organism (species, biotype and serotype)		Source/Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
	non-O:1,non-O:139 (O:7)	BEI NR-152	2.4×10^4	3xLoD
	O:1 Inaba, Biotype El Tor	ATCC 25870	2.4×10^4	3xLoD
Vibrio parahaemolyticus		ATCC 17802[a]	8.0×10^4	1xLoD
		ATCC BAA-242	2.4×10^5	3xLoD
		ATCC 27969	2.4×10^5	3xLoD
		ATCC 33845	2.4×10^5	3xLoD
		BEI NR-21990	2.4×10^5	3xLoD
		BEI NR-21992	2.4×10^5	3xLoD
Vibrio vulnificus		ATCC 29306	2.4×10^5	3xLoD
		ATCC 33817	2.4×10^5	3xLoD
		ATCC BAA-88	2.4×10^5	3xLoD
		ATCC 27562	2.4×10^4	0.3xLoD
		ATCC BAA-86	2.4×10^4	0.3xLoD

[a] Isolate was used to establish the LoD for this assay.

Note: In the clinical evaluation, a *Vibrio* carrying a variant *toxR* sequence was not detected by the Vchol assay and very rare strains of pathogenic *V. cholerae* that do not carry that *toxR* gene will also not be detected by the Vchol assay.

Table 20. FilmArray *Yersinia enterocolitica* Inclusivity Results

Organism	Serotype	Source/Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Yersinia enterocolitica	O:8	ATCC 9610[a]	5.0×10^4	1xLoD
		ATCC 23715	1.5×10^5	3xLoD
		BEI NR-207	1.5×10^5	3xLoD
	O:5, 27	NCTC 10463	1.5×10^5	3xLoD
	O:3	ATCC 700822	1.5×10^5	3xLoD
		BEI NR-212	1.5×10^5	3xLoD
	O:9	ATCC 55075	1.5×10^5	3xLoD

[a] Isolate was used to establish the LoD for this assay. The organism was quantified in CFU/mL by plate enumeration.

Note: In addition to those evaluated in this study, *in silico* sequence analysis indicates the FilmArray *Yersinia enterocolitica* assay should react with all strains/serotypes of *Y. enterocolitica* (including O:1, 2a, 3; O:2a,3; O:4,32; O:12,25; O:13a,13b; O:19; O:20; and O:21).

Table 21. FilmArray Enteroaggregative *E. coli* (EAEC) Inclusivity Results

Organism	Serotype	Source/Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Enteroaggregative *E. coli* (EAEC)	O92:H33	STEC Center JM221[a]	1.0×10^4	1xLoD
	O162:NM	Penn State 92.0148	3.0×10^4	3xLoD
	O17:H6	Penn State 92.0142	3.0×10^4	3xLoD
	O4:H7	Penn State 92.0144	3.0×10^4	3xLoD
	O51:H11	Penn State 92.0143	3.0×10^4	3xLoD
	O68:NM	Penn State 92.0154	3.0×10^4	3xLoD
	O7:NM	Penn State 92.0151	3.0×10^3	0.3xLoD
	O44:H18	STEC Center O42	3.0×10^3	0.3xLoD
	O104:H4 (Purified DNA)[b]	2011 European Outbreak strain[c]	3.0×10^3	0.3xLoD
	Ond:H10[d]	STEC Center 101-1	1.5×10^8	Not Detected[d]

[a] Isolate was used to establish the LoD for this assay. The organism was quantified in CFU/mL by plate enumeration.
[b] Purified DNA was quantified in GE/mL by spectrophotometer.
[c] Isolate has genetic characteristics consistent with STEC and EAEC.
[d] Phenotypic EAEC but known to not carry the marker(s) detected by the FilmArray GI Panel EAEC assay.

Table 22. FilmArray Enteropathogenic *E. coli* (EPEC) Inclusivity Results

Organism	Serotype	Typical/ Atypical	Source/Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Enteropathogenic *E. coli* (EPEC)	O127:H6	Typical	STEC Center E2348/69[a]	1.0×10^3	1×LoD
	O128:H2	Atypical	STEC Center DEC11a	3.0×10^3	3×LoD
	111a:NM	Unknown	STEC Center Stoke W	3.0×10^3	3×LoD
	O142:H6	Typical	STEC Center E851/71	3.0×10^3	3×LoD
	O55:H7	Atypical	STEC Center DEC5A	3.0×10^3	3×LoD
	O114:H2	Typical	STEC Center 3448-87	3.0×10^3	3×LoD
	O119:H+	Unknown	STEC Center RN410/1	3.0×10^3	3×LoD
	O96:H	Unknown	STEC Center HSP19/4	3.0×10^3	3×LoD
	O86:Hnm	Unknown	STEC Center E990	3.0×10^3	3×LoD
	O55:H-	Unknown	STEC Center MA551/1	3.0×10^3	3×LoD

[a] Isolate was used to establish the LoD for this assay. The organism was quantified in CFU/mL by plate enumeration.

Table 23. FilmArray Enterotoxigenic *E. coli* (ETEC) *lt/st* Inclusivity Results

Organism	Serotype	ST/LT	Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Enterotoxigenic *E. coli* (ETEC)	O78:H11	STA (+)/LT (+)	ATCC 35401[a]	1.0×10^3	1×LoD
	O175:H15	STA (-)/LT (+)	Penn State 6.0671	3.0×10^3	3×LoD
	O149:H5	STA (-)/LT (+)	Penn State 6.1182	3.0×10^3	3×LoD
	O84:H28	STA (-)/LT (+)[b]	Penn State 7.1493	3.0×10^3	Not Detected[b]
	H5	STA (+)/LT (-)	Penn State 10.0049	3.0×10^3	3×LoD
	O168	STA (+)/LT (-)	Penn State 9.1809	3.0×10^3	3×LoD
	O145:H25	STA (+)/LT (-)	Penn State 10.0136	1.0×10^4	100xLoD[c]
	O78	STA (+)/LT (+)	Penn State 2.1507	3.0×10^3	3×LoD
	O19:H5	STA (+)/LT (+)	Penn State 5.0038	3.0×10^3	3×LoD
	H14	STA (+)/LT (-)	Penn State 10.045	3.0×10^3	3×LoD
	O141	STA (+)/LT (+)	Penn State 93.0045	3.0×10^3	3×LoD
	Unknown	STB (+)[d] STA(-)/LT(-)	Penn State 8.2425	1.5×10^9	Not Detected[d]
	Unknown	STB (+)[d] STA(-)/LT(-)	Penn State 9.1179	1.5×10^9	Not Detected[d]

[a] Isolate was used to establish the LoD for this assay. The organism was quantified in CFU/mL by plate enumeration.
[b] Secondary PCR assay could not confirm the presence of the target gene(s) – plasmid/gene loss suspected.
[c] Sequencing of the target gene(s) identified sequence variation leading to reduced sensitivity for STA in this isolate.
[d] The FilmArray GI Panel will not detect phenotypic ETEC that that express only heat-stable toxin ST2/STB or heat-labile toxin LT-II.

Table 24. FilmArray Shiga-like toxin producing *E. coli* (STEC) *stx1/stx2* and *E. coli* O157 Inclusivity Results

Organism	Serotype	*stx1/stx2*	Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected STEC	Multiple of LoD Detected O157
Shiga-like toxin producing *E. coli* (STEC)	**STEC (non-O157)**					
	O25:H11	+/+	ATCC BAA-2196[a]	1.0×10^3	1×LoD	Not Detected
	O113:H21	+/+	ATCC BAA-177	3.0×10^3	3×LoD	Not Detected
	O45:H2	Unknown	STEC Center DEC11C	3.0×10^3	3×LoD	Not Detected
	O103:H2	+/Unknown	STEC Center 107-226	3.0×10^3	3×LoD	Not Detected
	O104:H21	-/+	STEC Center G5506	3.0×10^3	3×LoD	Not Detected
	O111:NM	+/+	STEC Center 95-3208	3.0×10^3	3×LoD	Not Detected
	O111:H2	-/+	STEC Center RD8	3.0×10^3	3×LoD	Not Detected
	O111:H8	+/+	STEC Center DEC8B	3.0×10^3	3×LoD	Not Detected
	O121:H19	Unknown	STEC Center F6173	3.0×10^3	3×LoD	Not

Organism	Serotype	*stx1*/*stx2*	Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected STEC	Multiple of LoD Detected O157
						Detected
	O26:NM	+/-	STEC Center DA-22	3.0×10^3	3×LoD	Not Detected
	O26:H11	+/-	STEC Center H19	3.0×10^3	3×LoD	Not Detected
	O145:NM	+/-	STEC Center GS G5578620	3.0×10^3	3×LoD	Not Detected
	0104:H4[b] (Purified DNA)[c]	-/+	ATCC BAA-2326D-5[b]	3.0×10^{3c}	3×LoD	Not Detected
	STEC O157					
	O157:NM	+/+	STEC Center DA-26	3.0×10^3	3×LoD	0.3×LoD
	O157:H7	-/+	STEC Center E32511	3.0×10^3	3×LoD	0.3×LoD
	O157:HNT	+/+	STEC Center DA-74	3.0×10^3	3×LoD	0.3×LoD
	O157:H7	+/+	ATCC 43895[a]	1.0×10^4	10xLoD	1xLoD
	O157:H7	+/+	STEC Center A8993-CS2	3.0×10^4	30×LoD	3×LoD
	Non-STEC O157					
	O157:H7	-/-	ATCC 43888	3.0×10^4	Not Detected	N/A[d]
	O157:H45	-/-	STEC Center SC373/2	3.0×10^4	Not Detected	N/A[d]

[a] Isolate was used to establish the LoD. The organism was quantified in CFU/mL by plate enumeration.
[b] 2011 European Outbreak Strain. Isolate has genetic characteristics consistent with STEC and EAEC.
[c] Purified DNA was quantified in GE/mL by spectrophotometer.
[d] *E. coli* O157 N/A results reported due to lack of positive results for STEC.

Note: Based on *in silico* analysis, *stx2* subtypes e and f are predicted to be detected with reduced sensitivity or not detected by the FilmArray GI Panel STEC assays.

Table 25. FilmArray Shigella/Enteroinvasive *E. coli* (EIEC) Inclusivity Results

Organism	Serotype (Temporal/Geographic Isolation)	Source/Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Enteroinvasive *E. coli* (EIEC)	O29:NM	ATCC 43892[a]	5.0×10^3	1×LoD
	O29:HNM (1977)	STEC Center 1885-77	3.0×10^3	0.6×LoD
	O124:HNM (1978)	STEC Center 929-78	3.0×10^3	0.6×LoD
	O29:H27 (USA, VA; 1979)	STEC Center 1827-79	3.0×10^3	Not Detected[b]
	O28:H- (Brazil, 1983)	STEC Center LT-15	3.0×10^3	0.6×LoD
	O136:H- (Bangladesh, 1983)	STEC Center LT-41 Strain 1111-55	3.0×10^3	0.6×LoD

Organism	Serotype (Temporal/Geographic Isolation)	Source/Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Shigella boydii (Serogroup C)	Type 2	ATCC 8700	3.0×10^2	3×LoD
	Type 4	CDPH HUM-2010029296	3.0×10^2	3×LoD
	Type 1	ATCC 9207	3.0×10^2	3×LoD
	Type 20	ATCC BAA-1247	3.0×10^2	3×LoD
	Type 10	ATCC 12030	3.0×10^2	3×LoD
Shigella dysenteriae (Serogroup A)	Type 1	BEI NR-520	3.0×10^2	3×LoD[c]
	Type 2	CDPH PHM-2004008089	3.0×10^2	3×LoD
	Type 13	ATCC 49555	3.0×10^2	3×LoD
	Type 3	ATCC 29028	3.0×10^2	3×LoD
	Type 12	ATCC 49551	3.0×10^2	3×LoD
Shigella flexneri (Serogroup B)	Type 2a	ATCC 700930	3.0×10^2	3×LoD
	Type 1a	ATCC 9199	3.0×10^2	3×LoD
	Type 6	CDPH PHM-2006004043	3.0×10^2	3×LoD
	Type 2b	ATCC 12022	3.0×10^2	3×LoD
	Type 2a	ATCC 29903	3.0×10^2	3×LoD
	Unknown	STEC Center VA-6	3.0×10^2	3×LoD
Shigella sonnei (Serogroup D)	N/A	ATCC 29930	1.0×10^{2a}	1×LoD
	N/A	ATCC 11060	3.0×10^2	3×LoD
	N/A	CDPH HUM-2010027998	3.0×10^2	3×LoD
	N/A	ATCC 29031	3.0×10^2	3×LoD
	N/A	ATCC 25931	3.0×10^2	3×LoD
	N/A	ATCC 9290	3.0×10^2	3×LoD

[a] Isolate was used to establish the LoD for this assay. The organism was quantified in CFU/mL by plate enumeration.
[b] Secondary PCR assay could not confirm the presence of the target gene(s) – plasmid/gene loss suspected.
[c] This isolate gave the expected STEC Detected and *Shigella*/EIEC Detected results due to the presence of *stx* in *Shigella dysenteriae*.

Table 26. FilmArray *Cryptosporidium* Inclusivity Results

Organism	Geographic Source/ Isolate	Concentration Detected (cells/mL)	Multiple of LoD Detected
Cryptosporidium canis	Peru Clinical Sample	Unknown	<LoD[a]
Cryptosporidium hominis	Scotland Clinical Sample[b]	$2.1 \times 10^{3\,b}$	1×LoD
	Scotland Clinical Sample	6.4×10^3	3×LoD
	Scotland Clinical Sample	6.4×10^3	3×LoD

Organism	Geographic Source/ Isolate	Concentration Detected (cells/mL)	Multiple of LoD Detected
	BEI NR-2520 (Purified DNA Isolate TU502)	6.4×10^3	3×LoD
Cryptosporidium meleagridis	BEI NR-2521 (Purified DNA Isolate TU1867)	1.8×10^3	3×LoD
Cryptosporidium muris	Waterborne P104	1.5×10^4 oocycts/mL	3×LoD
Cryptosporidium parvum	Waterborne P102C[c]	6.0×10^{2} [c]	1×LoD
	Scotland Clinical Sample	1.8×10^3	3×LoD
	Scotland Clinical Sample	1.8×10^3	3×LoD
	BEI NR-2519 (Purified DNA Isolate Iowa)	1.8×10^3	3×LoD
Cryptosporidium ubiquitum	Scotland Purified DNA from Clinical Sample	Unknown	<LoD[a]
	Scotland Purified DNA from Clinical Sample	Unknown	<LoD[a]

[a] Quantification by qPCR indicated that these purified samples have an analyte concentration that is lower than the assay LoD.
[b] This *C. hominis* sample was used to establish the LoD for *C. hominis* (LoD of 5.0×10^3 oocysts/mL was determined to be equivalent to 2.1×10^3 copies/mL).
[c] This *C. parvum* isolate was used to establish the LoD for *C. parvum* (LoD of 5.0×10^3 oocysts/mL was determined to be equivalent to 6.0×10^2 copies/mL).

Note: *In silico* sequence analysis indicates the FilmArray *Cryptosporidium* assay(s) should react with approximately 23 different *Cryptosporidium* species (including those evaluated in this study) as well as sequences not assigned to specific species. *In silico* analysis predicts that the *Cryptosporidium* assay(s) may not react with the rare or non-human species *C. bovis*, *C. ryanae* and *C. xiaoi*.

Table 27. FilmArray *Cyclospora cayetanensis* Inclusivity Results

Organism	Location/Sample		Concentration Detected (GE/mL)	Multiple of LoD Detected
Cyclospora cayetanensis	Nebraska	Clinical Specimen[a]	180	1×LoD
		Clinical Specimen	540	3×LoD
		Clinical Specimen	540	3×LoD
	Peru	Clinical Specimen	540	3×LoD
		Clinical Specimen	540	3×LoD
		Clinical Specimen	540	3×LoD
		Clinical Specimen	540	3×LoD

[a] Isolate was used to establish the LoD for this assay.

Table 28. FilmArray *Entamoeba histolytica* Inclusivity Results

Organism	Strain Designation	Location/Year of Isolation	Isolate ID	Concentration Detected (copies/mL)	Multiple of LoD Detected
Entamoeba histolytica	HM-1:IMSS	Mexico City 1967	ATCC 30459[a]	~1.2 x 10^5	1×LoD
	EntaHB-301:NIH	Burma 1960	BEI NR-176	3.6 x 10^5	3×LoD
	Rahman	England 1972	BEI NR-179	3.6 x 10^5	3×LoD
	HU-21:AMC	Arkansas 1970	BEI NR-2589	3.6 x 10^5	3×LoD
	IP:1182:2	Honduras 1982	BEI NR-20088	3.6 x 10^5	3×LoD
	SAW 408 RR, Clone A	Mexico	BEI NR-20090	3.6 x 10^5	3×LoD

[a] Isolate was used to establish the LoD for this assay (LoD of 2.0×10^3 cells/mL was determined to be equivalent to ~1.2×10^5 copies/mL).

Table 29. FilmArray *Giardia lamblia* Inclusivity Results

Organism	Location/Year of Isolation	Isolate ID	Concentration Detected (cells/mL)	Multiple of LoD Detected
Giardia lamblia (aka *G. intestinalis* or *G. duodenalis*)	New Orleans, LA 1985	ATCC 50137	150	3×LoD
	Portland, OR 1971	ATCC 30888	150	3×LoD
	Bethesda, MD 1979	ATCC 30957[a]	50	1×LoD
	Unknown	Waterborne P101	150	3×LoD
	Egypt	ATCC PRA-243	150	3×LoD
	United States	ATCC PRA-247	150	3×LoD

[a] Isolate was used to establish the LoD for this assay.

Table 30. FilmArray Adenovirus F 40/41 Inclusivity Results

Organism	Source/ Isolate ID	Concentration Detected (copies/mL)	Multiple of LoD Detected
Adenovirus F 40	ATCC VR-931[a]	~2.8×10^5	1×LoD
	Clinical Sample E239	8.4×10^5	3×LoD
	NCPV 0101141v (Dugan)	8.4×10^5	3×LoD
	Zeptometrix 0810084CF	8.4×10^5	3×LoD
Adenovirus F 41	ATCC VR-930 (Tak)[a]	~3.0×10^4	1×LoD
	Zeptometrix #0810085CF (Tak)[b]	9.0×10^4	10×LoD[b]
	UIRF/Zeptometrix 305571	9.0×10^4	3×LoD
	Clinical Sample 762	9.0×10^4	3×LoD
	Clinical Sample 976	9.0×10^4	3×LoD
	Clinical Sample Chn81	9.0×10^4	3×LoD

[a] Isolate was used to establish the LoD for this assay. For ATCC VR-9310, the LoD of 1 $TCID_{50}$/mL was determined to be equivalent to 2.8×10^5copies/mL and for ATCC VR-930, the LoD of 100 $TCID_{50}$/mL was determined to be equivalent to 3.0×10^4copies/mL.
[b] Same strain as ATCC VR-930 (which was detected at 1× LoD) but obtained from a different source.

Table 31. FilmArray Astrovirus Inclusivity Results

Organism	Type	Location/Source/Isolate ID	Concentration Detected (copies/mL)	Multiple of LoD Detected
Human Astrovirus	1	China Clinical Sample	3.9×10^7	10×LoD
		China Clinical Sample	3.9×10^7	3×LoD
	2	USA Clinical Sample	3.9×10^7	3×LoD
	3	University of Barcelona Spain	3.9×10^7	3×LoD
	4	NCPV #1002072v	3.9×10^7	3×LoD
	5	USA Clinical Sample	3.9×10^7	3×LoD
		USA Clinical Sample	3.9×10^7	3×LoD
	6	University of Barcelona Spain	3.9×10^7	3×LoD
	7	University of Barcelona Spain	3.9×10^7	3×LoD
	8	NCPV #1003071v[a]	~1.3×10^7	1×LoD

[a] Isolate was used to establish the LoD for this assay (LoD of 50 FFU/mL was determined to be equivalent to1.3×10^7 copies/mL).

Table 32. FilmArray Norovirus GI/GII Inclusivity Results

Norovirus Genogroup/Genotype		Isolate ID (Clinical Samples)	Concentration Detected (copies/mL)	Multiple of LoD Detected
Norovirus GI	3	Noro1_036[a]	1.0×10^4	1×LoD
	2	Noro1_002	6.0×10^3	0.6×LoD
	3	Noro1_003	6.0×10^3	0.6×LoD
		Noro1_012	6.0×10^3	0.6×LoD
		Noro1_030	6.0×10^3	0.6×LoD
	4	Noro1_031	6.0×10^3	0.6×LoD
	6	Noro1_021	1.0×10^5	10×LoD
	7	Noro1_009	2.0×10^5	20×LoD[c]
		Noro1_029	6.0×10^3	0.6×LoD
		Noro1_034	6.0×10^3	0.6×LoD
	8	Noro G1.8[b]	6.0×10^4	6×LoD
Norovirus GII	Unknown	Noro2_013[a]	1.0×10^4	1×LoD
	2	NoroII.2[b]	6.0×10^3	0.6×LoD
	3	China-5	6.0×10^3	0.6×LoD
		SGB_038	6.0×10^3	0.6×LoD
	4	GI-PILOT-SPDRL-077	2.0×10^5	20×LoD[c]
		Noro2_004	2.0×10^5	20×LoD[c]
		Noro2_032	2.0×10^5	20×LoD[c]
		PCMC_025 (Sydney)	6.0×10^3	0.6×LoD
		PCMC_031 (Sydney)	6.0×10^3	0.6×LoD
	6	NYH-A	6.0×10^3	0.6×LoD
	7	NoroII.7[b]	6.0×10^3	0.6×LoD
	8	NoroII.8[b]	6.0×10^3	0.6×LoD
	12	NoroII.12[b]	6.0×10^3	0.6×LoD
	16	NoroII.16[b]	6.0×10^3	0.6×LoD
	20	NoroII.20c[b]	2.0×10^5	20×LoD[c]
		NoroII.20[b]	6.0×10^3	0.6×LoD

[a] Isolate was used to establish the LoD for this assay.
[b] Isolate obtained as RNA extract from a clinical sample. Genotype provided by the source laboratory.
[c] Noroviruses are genetically diverse. *In silico* analysis predicts that most strains of all genotypes will be detected, though some variant strains may be detected with reduced sensitivity or may not be detected due to inefficient amplification or exclusion by melt analysis.

Table 33. FilmArray Rotavirus A Inclusivity Results

Organism	Strain Designation (Serotype)	Isolate ID	Concentration Detected (copies/mL)	Multiple of LoD Detected
Rotavirus A	ST3 (G4P6)	NCPV 0904053v[a]	3.9×10^3	1×LoD
	RV4 (G1P8)	NCPV 0904052v	1.2×10^4	3×LoD
	69M (G8P5)	NCPV 0904055v	1.2×10^4	3×LoD
	P (G3P1A[8])	NCPV 0904056v	1.2×10^4	3×LoD
	Wa (G1P1A[8])	ATCC VR-2018	1.2×10^4	3×LoD
	DS-1 (G2P1B[4])	ATCC VR-2550	1.2×10^4	3×LoD

[a] Isolate was used to establish the LoD for this assay (LoD of 1.0×10^5 FFU/mL was determined to be equivalent to 3.9×10^3 copies/mL).

Note: The Rotavirus A assay will also detect reassortant viruses used in vaccine production.

Table 34. FilmArray Sapovirus Inclusivity Results

Organism	Genogroup	Isolate ID (Clinical Samples)	Concentration Detected (copies/mL)	Multiple of LoD Detected
Sapovirus	GI	AB_SaV_14[a]	5.0×10^6	1×LoD
	Unknown	China_56	1.5×10^7	3×LoD
	Unknown	AB_SaV_03	1.5×10^7	3×LoD
	Unknown	PCMC_54	1.5×10^7	3×LoD
	Unknown	SPDRL-006	1.5×10^7	3×LoD
	Unknown	SPDRL-099	1.5×10^7	3×LoD
	Unknown	SGB-MP-11	1.5×10^7	3×LoD
	GI	Sapo_03[b]	1.5×10^7	3×LoD
	GII	Sapo_06[b]	1.5×10^7	3×LoD
	GIV	Sapo_09[b]	1.5×10^7	3×LoD
	GV	Sapo_02[b]	1.5×10^7	3×LoD

[a] Clinical Sample was used to establish the LoD for this assay.
[b] Isolate obtained as RNA extract from a clinical sample, genogroup information provided by source laboratory.

Exclusivity

The potential for cross-reactivity between assays contained in the FilmArray GI Panel was evaluated by testing high concentrations of analyte in contrived stool samples. The organisms/viruses tested consisted of on-panel (identified by the GI Panel assays) and off-panel (not identified by the GI Panel assays) organisms/viruses.

On-panel organisms were tested to verify that they only react with the appropriate assays on the panel. On-panel exclusivity testing included 28 analytes were selected to evaluate the potential for cross-reactivity with other panel assays. This group of organisms was chosen such that at least one positive result would be obtained for each assay in the FilmArray GI Panel. Each organism was tested at a high concentration to show analytical specificity with all FilmArray GI Panel assays.

Organisms for off-panel testing were selected based on a combination of several factors including (1) relatedness to specific species detected by the GI Panel (near-neighbors), (2) clinical relevance, (3) likelihood of being present in stool specimens and (4) genetic similarity to GI Panel assay primers, as determined by *in silico* analyses during assay design. When empirical testing of these organisms was not performed, a separate organism-specific *in silico* analysis of whole genome sequence(s) directed against all GI Panel primers was attempted for reactivity predictions.

Results are presented for all organisms/viruses that were tested and received the expected FilmArray GI Panel test result(s) (no cross-reactivity, Table 35), followed by a summary of organisms/viruses with which cross-reactivity was observed (Table 36).

Table 35. No Cross-Reactivity with FilmArray GI Panel Assays Observed or Predicted by *in silico* Analysis (Off-Panel Organisms)

BACTERIA				
Tested				
Abiotrophia defectivia	*Campylobacter mucosalis*	*Desulfovibrio piger*	*Klebsiella oxytoca*	*Ruminococcus flavefaciens*[a]
Acinetobacter baumannii	*Campylobacter rectus*	Diffusely adherent *E.coli*	*Klebsiella pneumoniae*	*Ruminococcus obeum*[a]
Acinetobacter lwoffii	*Campylobacter showae*	*Escherichia blattae*	*Lactobacillus acidophilus*	*Selenomonas ruminantium*
Aeromonas hydrophila	*Campylobacter sputorum*	*Escherichia fergusonii*	*Lactobacillus reuteri*	*Serratia liquefaciens*
Alcaligenes faecalis	*Campylobacter ureolyticus*	*Escherichia hermannii*	*Lactococcus lactis*	*Serratia marcescens*
Anaerococcus tetradius	*Cedecea davisae*[b]	*Escherichia vulneris*	*Leminorella grimontii*	*Shewanella algae*
Arcobacter butzleri	*Chlamydia trachomatis*	*Edwardsiella tarda*	*Listeria monocytogenes*	*Staphylococcus aureus*
Arcobacter cryaerophilus	*Citrobacter amalonaticus*	*Egglerthella lenta*	*Megamonas hypermegale*	*Staphylococcus epidermidis*
Bacillus cereus	*Citrobacter freundii*	*Enterobacter aerogenes*	*Megasphaeara elsdenii*	*Stenotrophomonas maltophilia*
Bacteroides fragilis	*Clostridium acetobutylicum*	*Enterobacter cloacae*	*Methanobrevibacter smithii*	*Streptococcus agalactiae*
Bacteroides thetaiotaomicron	*Clostridium botulinum*	*Enterococcus faecalis*	*Morganella morganii*	*Streptococcus intermedius*
Bacteroides vulgatus	*Clostridium difficile* non-toxigenic[c]	*Enterococcus faecium*	*Peptoniphilus asaccharolyticus*	*Streptococcus pyogenes*
Bifidobacterium adolescentis[a]	*Clostridium histolyticum*	*Eubacterium cylindroides*	*Peptostreptococcus anaerobius*	*Streptococcus salivarius*
Bifidobacterium bifidum[a]	*Clostridium methylpentosum*	*Eubacterium rectale*	*Photobacterium damselae*	*Streptococcus suis*
Bifidobacterium longum[a]	*Clostridium novyi*	*Faecalibacterium prausnitzii*	*Porphyromonas asaccharolytica*	*Trabulsiella guamensis*
Campylobacter concisus	*Clostridium perfringens*	*Fusobacterium varium*	*Prevotella melaninogenica*	*Veillonella parvula*
Campylobacter curvus	*Clostridium ramosum*	*Gardnerella vaginalis*	*Proteus mirabilis*	*Yersinia bercovieri*
Campylobacter fetus	*Clostridium septicum*	*Gemella morbillorum*	*Proteus penneri*	*Yersinia frederiksenii*[d]
Campylobacter gracilis	*Clostridium sordellii*	*Haemophilus influenzae*	*Proteus vulgaris*	*Yersinia intermedia*
Campylobacter helveticus	*Clostridium tetani*	*Hafnia alvei*[b]	*Provedencia alcalifaciens*	*Yersinia mollaretii*
Campylobacter hominis	*Collinsella aerofaciens*	*Helicobacter fennelliae*	*Pseudomonas aeruginosa*	*Yersinia pseudotuberculosis*
Campylobacter hyointestinalis	*Corynebacterium genitalium*	*Helicobacter pylori*	*Ruminococcus bromii*[a]	*Yersinia rohdei*
Campylobacter lari				

PROTOZOA/PARASITES				FUNGI
Tested		***In silico* Analysis Only**		**Tested**
Babesia microti	*Entamoeba moshkovskii*	*Ancylostoma duodenale*	*Entamoeba hartmanni*	*Aspergillus fumigatus*
Blastocystis hominis	*Giardia muris*	*Ascaris lumbricoides*	*Entamoeba polecki*	*Candida albicans*
Conidiobolus lachnodes	*Pentatrichomonas hominis*	*Balantidium coli*	*Enterobius vermicularis*	*Candida catenulate*
Conidiobolus lobatus	*Schistosoma mansoni*	*Chilomastix mesnili*	*Enteromonas hominis*	*Penicillium marneffei*
Encephalitozoon hellem	*Toxoplasma gondii*	*Dientamoeba fragilis*	*Isospora belli*	*Saccharomyces boulardi*
Encephalitozoon intestinalis	*Trichomonas tenax*	*Endolimax nana*	*Necator americanus*	*Saccharomyces cerevisiae*
Entamoeba gingivalis		*Entamoeba coli*		

VIRUSES				
Tested				***In silico* Analysis Only**
Adenovirus A:31	Adenovirus E:4a	Coronavirus 229E	Enterovirus 68	Adenovirus G52
Adenovirus B:34	Astrovirus variant VA1	Coxsackievirus B3	Hepatitis A	Norovirus GIV
Adenovirus C:2	Astrovirus variant MLB	Cytomegalovirus (CMV)	Herpes Simplex Type 2	Rotavirus B
Adenovirus D:37	Bocavirus Type 1	Echovirus 6	Rhinovirus 1A	Rotavirus C

[a] Though not observed in this study, cross-reactivity of the *Giardia lamblia* assay with one or more *Bifidobacterium* and *Ruminococcus* species was observed in the clinical evaluation. *Bifidobacterium* and *Ruminococcus* species are listed as potential cross-reacting organisms in Table 36.
[b] Though not observed in this study, possible cross-reactivity of the ETEC 2 assay with *Hafnia alvei* and *Cedeceae davisiae* was observed in the clinical evaluation or predicted by *in silico* analysis. *Halfnia alvei* and *Cedeceae davisiae* are also listed as potentially cross-reactive organisms in Table 36.
[c] Two isolates of this species were tested for analytical specificity.
[d] Though not observed in this study, i*n silico* analysis indicates that cross-reactivity between *Yersinia fredricksenii* and the *Yersinia entercolitica* assay is possible at high concentrations. *Y. fredricksenii* is also listed as potentially cross-reactive organism in Table 36.

Table 36. Observed or Predicted Cross-Reactivity between GI Panel Assays and Off-Panel Organisms

FilmArray GI Panel Test Result	Cross-Reactive Organism(s)
Entamoeba histolytica	*Entamoeba dispar*
Giardia lamblia	*Bifidobacterium* spp.[a] *Ruminococcus* spp.[a]
Enterotoxigenic *E.coli* (ETEC) *lt/st* [ETEC 2 assay]	*Citrobacter koseri* *Citrobacter sedlakii* *Hafnia alvei*[a] *Cedeceae davisiae*[a]
Salmonella[b]	*E. coli* with variant type III secretion protein[b]
Vibrio (*V. parahaemolyticus/V. vulnificus/ V. cholerae*)	*Vibrio alginolyticus* *Vibrio fluvialis*[c] *Vibrio mimicus*[c] *Grimontia* (formerly *Vibrio) hollisae*
Yersinia enterocolitica	*Yersinia frederiksenii*[a,d] *Yersinia kristensenii*[d]

[a] Cross-reactivity was not observed when tested at high concentration (1.5×10^9 cells/mL). However, cross reactivity was suspected or confirmed in clinical specimens and/or the potential for cross-reactivity is supported by *in silico* predictions.
[b] Cross-reactivity resulting in false positive *Salmonella* results has not been observed in analytic or clinical testing. However, non-specific amplification products with Tm values close to the assay specific Tm range have been observed and the potential for false positive *Salmonella* test results exists.
[c] Detected at concentrations near the *Vibrio* assay LoD.
[d] *Y. kristensenii* and *Y. fredericksenii* are difficult to distinguish from *Y. entercolitica* by standard laboratory methods.

Interference

Substances that could be present in stool samples (preserved in Cary Blair transport medium) or introduced during sample handling were evaluated for their potential to interfere with assay performance. A potentially interfering substance (see Tables 37 – 39) was added to a contrived stool sample by spiking representative GI Panel organisms into negative sample matrix (individual or pooled donor stool in transport medium). Each contrived sample contained a mix of four different organisms, each present at approximately three times (3×) the limit of detection (LoD). Contrived samples without added potentially interfering substances served as positive controls.

Of the endogenous and exogenous substances tested (Table 37), only the bovine-derived mucin gave unexpected results (EPEC was reported in samples that were not spiked with EPEC). An investigation found bacterial nucleic acid in the bovine-derived mucin used as the test substance, and it was determined that the unexpected results were due to EPEC contamination in the commercially prepared mucin.

Table 37. Potentially Interfering Endogenous and Exogenous Substances Tested

Endogenous Substances	Exogenous Substances (including laboratory disinfectants)	
Human Whole Blood	Bacitracin	Glycerin
Triglycerides	Doxycycline	Hydrocortisone
Cholesterol	Nystatin	Loperamide hydrochloride
Fatty acids (palmitic acid)	Metronidazole	Magnesium hydroxide
Fatty acids (stearic acid)	Naproxen sodium	Mineral oil
Bovine Mucin [a]	Bisacodyl	Phenylephrine hydrochloride
Human Bile	Bismuth subsalicylate	Sodium phosphate
Human Urine	Calcium carbonate	Nonoxynol-9
Human stool (overfill of Cary Blair vial)	Docusate sodium	Bleach
		Ethanol

[a] Unexpected EPEC detected results reported. The presence of EPEC nucleic acid in test material was confirmed by independent PCR assays, indicating the unexpected results were caused by contamination of the mucin with EPEC.

No inhibition or unexpected test results were obtained in the presence of high concentrations of potentially competing microorganisms (on-panel or off-panel organisms; Table 38). However, Rotavirus A Detected results were reported when Rotavirus A reassortant strains used in the manufacturing of Rotavirus A vaccines were tested (Table 38). Rotavirus A vaccine may be shed in stool following oral administration and Rotavirus A will be detected by the FilmArray GI Panel if vaccine is present in the test sample.

Table 38. Potentially Interfering or Competing Organisms and Vaccine Material Tested

Off-Panel Organisms	On-Panel Organisms
Aeromonas hydrophila	Adenovirus F41
Bacteroides vulgatus	Enterotoxigenic *E. coli* (ETEC)
Bifidobacterium bifidum	
Human Rhinovirus 87	
Non-pathogenic *E. coli*	**RotaTeq Rotavirus A Vaccine Components**
Helicobacter pylori	Rotavirus reassortant WC3:2-5, R574(9) [ATCC VR-2195][a]
Saccharomyces boulardii	Rotavirus reassortant WI79-4,9 [ATCC VR-2415][a]

[a] Reactivity with the FilmArray Rotavirus A assay expected.

Contrived stool samples prepared in various enteric and fixative-containing transport media, including Cary Blair (see Table 39), were evaluated for the potential of different media to interfere with the accuracy of FilmArray GI Panel test results. No interference was observed for samples collected in Protocol Cary Blair or other brands of enteric transport media (Para-Pak Enteric Plus and Para-Pak C&S media; performance of the FilmArray GI Panel has not been established in these media). However, accurate detection of analytes was impaired (false negative results) for samples prepared in media containing fixatives, particularly those containing formalin.

Table 39. Transport Media Tested

Enteric Transport Media – No Interference Observed		
PROTOCOL™ Cary Blair	Para-Pak Enteric Plus[a]	Para-Pak C&S[a]
Fixative-containing Transport Media – Interference Observed[a]		
Modified (Cu) PVA Fixative	Para-Pak 10% Formalin Fixative[b]	Para-Pak SAF Fixative[a]
Para-Pak ECOFIX Fixative	Para-Pak LV-PVA Fixative	Para-Pak Zn-PVA Fixative

[a]Performance has not been established in these media
[b]Impaired detection of analytes (false negative results) observed in formalin containing media.

Reproducibility

A multicenter reproducibility study was performed to determine between-site and overall reproducibility of the FilmArray GI Panel. Reproducibility testing occurred at three test sites using a panel of contrived stool samples, each spiked with various combinations of four different GI Panel analytes. Each analyte was evaluated at three different concentrations (Negative, Low Positive and Moderate Positive).

The study incorporated a range of potential variation introduced by 13 different operators, 4 different pouch lots, and 16 different FilmArray Instruments. Samples were stored refrigerated (4°C) or frozen (≤-70°C) prior to testing. Frozen samples were tested on five different days at three testing sites for 90 data points per sample and refrigerated samples were tested on four different days at three testing sites for 108 data points per sample. A summary of results (percent (%) agreement with the expected result) for each

analyte (by site and overall) is provided in Table 40. The reproducibility of Tm for each positive assay is provided in the Table 41.

Table 40. Reproducibility of the FilmArray GI Panel Test Results

Organism Tested	Concentration Tested	Expected Result	% Agreement with Expected Result			
			Site A	Site B	Site C	All Sites (95% Confidence Interval)
Campylobacter jejuni ATCC BAA-1234	**Moderate Positive** 3xLoD $1.2x10^5$ cells/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	Low Positive 1xLoD $4x10^4$ cells/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	None	Not Detected	192/192 100%	192/192 100%	192/192 100%	576/576 100% (99.4 - 100%)
Clostridium difficile[a] ATCC 9689	**Moderate Positive** 3xLoD $1.2x10^6$ cells/mL	Detected	36/36 100%	36/36 100%	36/36 100%	108/108 100% (96.6 - 100%)
	Low Positive 1xLoD $4x10^5$ cells/mL	Detected	36/36 100%	36/36 100%	36/36 100%	108/108 100% (96.6 - 100%)
	None	Not Detected	120/120 100%	120/120 100%	120/120 100%	360/360 100% (96.6 - 100%)
Escherichia coli **(EPEC)** E2348/69 (STEC Center, MSU)	**Moderate Positive** 3xLoD $3x10^3$ CFU/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	Low Positive 1xLoD $1x10^3$ CFU/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	None	Not Detected	192/192[b] 100%	192/192[b] 100%	192/192[b] 100%	576/576 100% (99.4 - 100%)
Salmonella enterica[a] SarC1 (SGSC)	**Moderate Positive** 3xLoD $1.5x10^4$ CFU/mL	Detected	36/36 100%	36/36 100%	36/36 100%	108/108 100% (96.6 - 100%)
	Low Positive 1xLoD $5x10^3$ CFU/mL	Detected	36/36 100%	36/36 100%	36/36 100%	108/108 100% (96.6 - 100%)
	None	Not Detected	120/120 100%	120/120 100%	120/120 100%	360/360 100% (96.6 - 100%)

Organism Tested	Concentration Tested	Expected Result	% Agreement with Expected Result			
			Site A	Site B	Site C	All Sites (95% Confidence Interval)
***Escherichia coli* (STEC) O157** ATCC 43895	**Moderate Positive** 3xLoD $3x10^4$ CFU/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	Low Positive 1xLoD $1x10^4$ CFU/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	None	N/A	192/192 100%	192/192 100%	192/192 100%	576/576 100% (99.4 - 100%)
Shigella sonnei ATCC 29930	**Moderate Positive** 3xLoD $3x10^2$ CFU/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	Low Positive 1xLoD $1x10^2$ CFU/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	None	Not Detected	192/192 100%	192/192 100%	192/192 100%	576/576 100% (99.4 - 100%)
Vibrio parahaemolyticus[a] ATCC 17802	**Moderate Positive** 3xLoD $2.4x10^5$ cells/mL	Detected	36/36 100%	36/36 100%	36/36 100%	108/108 100% (96.6 - 100%)
	Low Positive 1xLoD $8x10^4$ cells/mL	Detected	36/36 100%	36/36 100%	36/36 100%	108/108 100% (96.6 - 100%)
	None	Not Detected	120/120 100%	120/120 100%	120/120 100%	360/360 100% (96.6 - 100%)
Cryptosporidium parvum Waterborne P102C	**Moderate Positive** 3xLoD $1.5x10^4$ oocysts/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	Low Positive 1xLoD $5x10^3$ oocysts/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	None	Not Detected	192/192 100%	192/192 100%	192/192 100%	576/576 100% (99.4 - 100%)
Giardia intestinalis[a] (syn. *Giardia lamblia*)	**Moderate Positive** 3x LoD 150 cells/mL	Detected	36/36 100%	36/36 100%	36/36 100%	108/108 100% (96.6 - 100%)

Organism Tested	Concentration Tested	Expected Result	% Agreement with Expected Result			
			Site A	Site B	Site C	All Sites (95% Confidence Interval)
ATCC 30957	**Low Positive** 1xLoD 50 cells/mL	Detected	30/36 83.3%	30/36 83.3%	31/36 86.1%	91/108 84.3% (77.0 - 91.0%)
	None	Not Detected	120/120 100%	120/120 100%	120/120 100%	360/360 100% (96.6 - 100%)
Adenovirus F41 ATTC VR-930	**Moderate Positive** 3x LoD 300 $TCID_{50}$/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	Low Positive 1xLoD 100 $TCID_{50}$/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	None	Not Detected	192/192 100%	192/192 100%	192/192 100%	576/576 100% (99.4 - 100%)
Astrovirus (Type 8) NCPV 1003071v	**Moderate Positive** 3xLoD 150 FFU/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	Low Positive 1xLoD 50 FFU/mL	Detected	30/30 100%	30/30 100%	30/30 100%	90/90 100% (96.0 - 100%)
	None	Not Detected	192/192 100%	192/192 100%	192/192 100%	576/576 100% (99.4 - 100%)
Norovirus GI Clinical Specimen	**Moderate Positive** 3xLoD $3x10^4$ copies/mL	Detected	29/30 96.7%	30/30 100%	30/30 100%	89/90 98.9% (96.0 - 100%)
	Low Positive 1xLoD $1x10^4$ copies/mL	Detected	28/30 93.3%	29/30 96.7%	30/30 100%	87/90 96.7% (96.0 - 100%)
	None	Not Detected	192/192 100%	192/192 100%	192/192 100%	576/576 100% (99.4 - 100%)

[a] Reproducible, but suboptimal (<95%) detection was observed at one or both concentrations in frozen contrived samples. Data presented are from contrived samples stored at ~4°C for up to 4 days prior to testing.

[b] Includes N/A results for 60 samples (180 for all sites) spiked with STEC O157. When an STEC is detected, N/A is reported for the EPEC test result, regardless of the status of the EPEC assay.

The reproducibility of Tm for each positive assay was also evaluated and a summary is provided in the following table.

Table 41. Reproducibility of Tm for Positive FilmArray GI Panel Assays

Organism	Assay		Test Level	Test Site	Tm Reproducibility				
					Mean	StDev Tm	Min	Max	(Max - Min)
Bacteria and (Including Diarrheagenic *E. coli*)									
Campylobacter jejuni ATCC BAA-1234	Campy 1		Moderate Positive 3xLoD $1.2x10^5$ cells/mL	Site A	78.38	± 0.27	77.86	79.01	1.15
				Site B	78.28	± 0.21	77.87	78.59	0.72
				Site C	78.04	± 0.29	77.60	78.59	0.99
				All Sites	78.23	± 0.30	77.60	79.01	1.41
			Low Positive 1xLoD $4x10^4$ cells/mL	Site A	78.60	± 0.33	77.73	79.47	1.74
				Site B	78.65	± 0.19	78.28	79.01	0.73
				Site C	78.21	± 0.26	77.73	78.72	0.99
				All Sites	78.48	± 0.33	77.73	79.47	1.74
Clostridium difficile ATCC 9689	Cdiff[a]	Tm 1	Moderate Positive 3xLoD $1.2x10^6$ cells/mL	Site A	76.01	± 0.34	75.30	76.99	1.69
				Site B	75.79	± 0.40	74.71	76.59	1.88
				Site C	75.60	± 0.34	75.02	77.09	2.07
				All Sites	75.80	± 0.39	74.71	77.09	2.38
			Low Positive 1xLoD $4x10^5$ cells/mL	Site A	76.18	± 0.43	75.45	77.15	1.70
				Site B	75.94	± 0.43	75.09	76.74	1.65
				Site C	75.73	± 0.28	75.29	76.45	1.16
				All Sites	75.95	± 0.43	75.09	77.15	2.06
		Tm 2	Moderate Positive 3xLoD $1.2x10^6$ cells/mL	Site A	78.84	± 0.26	78.44	79.56	1.12
				Site B	78.61	± 0.30	77.86	79.17	1.31
				Site C	78.40	± 0.22	78.01	79.02	1.01
				All Sites	78.62	± 0.32	77.86	79.56	1.70
			Low Positive 1xLoD $4x10^5$ cells/mL	Site A	78.94	± 0.31	78.45	79.61	1.16
				Site B	78.67	± 0.30	78.02	79.17	1.15
				Site C	78.48	± 0.24	78.02	79.02	1.00
				All Sites	78.70	± 0.34	78.02	79.61	1.59
***Escherichia coli* (EPEC)** E2348/69 (STEC Center, MSU)	Ec eae		Moderate Positive 3xLoD $3x10^3$ CFU/mL	Site A	80.53	± 0.24	80.16	81.04	0.88
				Site B	80.39	± 0.20	79.86	80.74	0.88
				Site C	80.38	± 0.17	80.01	80.61	0.60
				All Sites	80.43	± 0.22	79.86	81.04	1.18
			Low Positive 1xLoD $1x10^3$ CFU/mL	Site A	80.59	± 0.24	80.15	81.18	1.03
				Site B	80.46	± 0.20	79.87	80.73	0.86
				Site C	80.42	± 0.14	80.15	80.72	0.57
				All Sites	80.49	± 0.21	79.87	81.18	1.31

Organism	Assay	Test Level	Test Site	Tm Reproducibility				
				Mean	StDev Tm	Min	Max	(Max - Min)
Salmonella enterica SarC1 (SGSC)	Salm	Moderate Positive 3xLoD $1.5x10^4$ CFU/mL	Site A	82.17	± 0.20	81.86	82.59	0.73
			Site B	81.88	± 0.26	81.30	82.32	1.02
			Site C	81.78	± 0.25	81.44	82.17	0.73
			All Sites	81.95	± 0.29	81.30	82.59	1.29
		Low Positive 1xLoD $5x10^3$ CFU/mL	Site A	82.21	± 0.27	81.74	82.77	1.03
			Site B	81.96	± 0.26	81.31	82.39	1.08
			Site C	81.83	± 0.25	81.45	82.31	0.86
			All Sites	82.00	± 0.30	81.31	82.77	1.46
Escherichia coli (STEC) O157 ATCC 43895	O157	Moderate Positive 3xLoD $3x10^4$ CFU/mL	Site A	83.23	± 0.22	82.58	83.77	1.19
			Site B	83.20	± 0.19	82.85	83.60	0.75
			Site C	82.96	± 0.29	82.59	83.44	0.85
			All Sites	83.13	± 0.26	82.58	83.77	1.19
		Low Positive 1xLoD $1x10^4$ CFU/mL	Site A	83.26	± 0.24	82.80	83.88	1.08
			Site B	83.20	± 0.20	82.73	83.59	0.86
			Site C	83.01	± 0.29	82.46	83.60	1.14
			All Sites	83.16	± 0.26	82.46	83.88	1.42
	STEC 1	Moderate Positive 3xLoD $3x10^4$ CFU/mL	Site A	82.85	± 0.25	82.16	83.48	1.32
			Site B	82.80	± 0.19	82.28	83.17	0.89
			Site C	82.52	± 0.28	82.16	83.02	0.86
			All Sites	82.72	± 0.28	82.16	83.48	1.32
		Low Positive 1xLoD $1x10^4$ CFU/mL	Site A	82.89	± 0.24	82.44	83.31	0.87
			Site B	82.78	± 0.18	82.44	83.17	0.73
			Site C	82.55	± 0.28	82.03	83.17	1.14
			All Sites	82.74	± 0.27	82.03	83.31	1.28
	STEC 2	Moderate Positive 3xLoD $3x10^4$ CFU/mL	Site A	84.99	± 0.22	84.44	85.49	1.05
			Site B	84.90	± 0.19	84.43	85.31	0.88
			Site C	84.68	± 0.30	84.30	85.16	0.86
			All Sites	84.86	± 0.27	84.30	85.49	1.19
		Low Positive 1xLoD $1x10^4$ CFU/mL	Site A	84.98	± 0.22	84.58	85.45	0.87
			Site B	84.92	± 0.19	84.45	85.30	0.85
			Site C	84.72	± 0.28	84.31	85.32	1.01
			All Sites	84.88	± 0.26	84.31	85.45	1.14
Shigella sonnei ATCC 29930	Shig	Moderate Positive 3xLoD $3x10^2$ CFU/mL	Site A	86.58	± 0.25	86.01	87.05	1.04
			Site B	86.38	± 0.19	85.87	86.61	0.74
			Site C	86.44	± 0.17	86.16	86.75	0.59
			All Sites	86.47	± 0.22	85.87	87.05	1.18
		Low Positive	Site A	86.57	± 0.22	86.29	87.18	0.89

Organism	Assay	Test Level	Test Site	Tm Reproducibility				
				Mean	StDev Tm	Min	Max	(Max - Min)
		1xLoD $1x10^2$ CFU/mL	Site B	86.52	± 0.24	86.02	87.01	0.99
			Site C	86.26	± 0.24	85.87	86.73	0.86
			All Sites	86.45	± 0.27	85.87	87.18	1.31
Vibrio parahaemolyticus ATCC 17802	Vibrio	Moderate Positive 3xLoD $2.4x10^5$ cells/mL	Site A	81.96	± 0.23	81.59	82.42	0.83
			Site B	81.69	± 0.24	81.02	82.03	1.01
			Site C	81.57	± 0.27	81.17	82.16	0.99
			All Sites	81.74	± 0.30	81.02	82.42	1.40
		Low Positive 1xLoD $8x10^4$ cells/mL	Site A	82.03	± 0.17	81.73	82.42	0.69
			Site B	81.74	± 0.23	81.29	82.17	0.88
			Site C	81.60	± 0.22	81.30	82.02	0.72
			All Sites	81.79	± 0.28	81.29	82.42	1.13
Protozoa								
Cryptosporidium parvum Waterborne P102C	Crypt 1	Moderate Positive 3xLoD $1.5x10^4$ oocysts/mL	Site A	78.99	± 0.23	78.58	79.46	0.88
			Site B	78.95	± 0.24	78.29	79.58	1.29
			Site C	78.83	± 0.15	78.57	79.16	0.59
			All Sites	78.92	± 0.22	78.29	79.58	1.29
		Low Positive 1xLoD $5x10^3$ oocysts/mL	Site A	79.00	± 0.26	78.59	79.61	1.02
			Site B	78.94	± 0.21	78.29	79.31	1.02
			Site C	78.88	± 0.18	78.43	79.17	0.74
			All Sites	78.95	± 0.23	78.29	79.61	1.32
	Crypt 2	Moderate Positive 3xLoD 1.5x104 oocysts/mL	Site A	71.75	± 0.28	71.29	72.31	1.02
			Site B	71.74	± 0.20	71.15	72.15	1.00
			Site C	71.50	± 0.20	71.28	72.15	0.87
			All Sites	71.67	± 0.26	71.15	72.31	1.16
		Low Positive 1xLoD $5x10^3$ oocysts/mL	Site A	71.81	± 0.35	71.29	72.43	1.14
			Site B	71.81	± 0.16	71.43	72.16	0.73
			Site C	71.59	± 0.21	71.28	72.14	0.86
			All Sites	71.74	± 0.27	71.28	72.43	1.15
Giardia intestinalis (syn. *G. lamblia*) ATCC 30957	Glam	Moderate Positive 3xLoD 150 cells/mL	Site A	91.52	± 0.24	91.04	92.08	1.04
			Site B	91.19	± 0.25	90.47	91.59	1.12
			Site C	91.12	± 0.29	90.62	91.74	1.12
			All Sites	91.28	± 0.31	90.47	92.08	1.61
		Low Positive 1xLoD 50 cells/mL	Site A	91.57	± 0.21	91.17	91.91	0.74
			Site B	91.24	± 0.22	90.75	91.62	0.87
			Site C	91.10	± 0.30	90.60	91.61	1.01
			All Sites	91.30	± 0.31	90.60	91.91	1.31
Viruses								

Organism	Assay	Test Level	Test Site	Tm Reproducibility				
				Mean	StDev Tm	Min	Max	(Max - Min)
Adenovirus F41 ATTC VR-930	**AdenoF**	**Moderate Positive 3xLoD 300 $TCID_{50}$/mL**	**Site A**	86.71	± 0.23	86.01	87.35	1.34
			Site B	86.61	± 0.18	86.28	87.03	0.75
			Site C	86.36	± 0.31	85.87	86.87	1.00
			All Sites	86.56	± 0.28	85.87	87.35	1.48
		Low Positive 1xLoD 100 $TCID_{50}$/mL	**Site A**	86.85	± 0.27	86.37	87.48	1.11
			Site B	86.70	± 0.20	86.30	87.16	0.86
			Site C	86.47	± 0.29	86.02	87.03	1.01
			All Sites	86.67	± 0.30	86.02	87.48	1.46
Astrovirus (Type 8) NCPV 1003071v	**Astro**	**Moderate Positive 3xLoD 150 FFU/mL**	**Site A**	85.62	± 0.25	85.17	86.06	0.89
			Site B	85.48	± 0.18	85.01	85.88	0.87
			Site C	85.51	± 0.21	85.02	85.90	0.88
			All Sites	85.54	± 0.22	85.01	86.06	1.05
		Low Positive 1xLoD 50 FFU/mL	**Site A**	85.67	± 0.26	85.17	86.19	1.02
			Site B	85.54	± 0.22	85.01	86.01	1.00
			Site C	85.55	± 0.16	85.29	85.89	0.60
			All Sites	85.59	± 0.22	85.01	86.19	1.18
Norovirus GI Clinical Specimen	**Noro 1**	**Moderate Positive 3xLoD $3x10^4$ copies/mL**	**Site A**	83.69	± 0.23	83.14	84.07	0.93
			Site B	83.46	± 0.20	82.92	83.76	0.84
			Site C	83.43	± 0.20	83.02	83.87	0.85
			All Sites	83.52	± 0.24	82.92	84.07	1.15
		Low Positive 1xLoD $1x10^4$ copies/mL	**Site A**	83.62	± 0.24	83.22	84.15	0.93
			Site B	83.59	± 0.21	83.18	83.98	0.80
			Site C	83.30	± 0.24	82.93	83.79	0.86
			All Sites	83.50	± 0.27	82.93	84.15	1.22

[a] A characteristic double melt profile is observed when both *C. difficile* toxin genes (tcdA and tcdB) are present in a sample and two different Tm values are reported (Tm1 and Tm2).

DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

Food and Drug Administration
10903 New Hampshire Avenue
Document Control Center – WO66-G609
Silver Spring, MD 20993-0002

BIOFIRE DIAGNOSTICS
BETH LINGENFELTER
390 WAKARA WAY
SALT LAKE CITY UT 84108

May 02, 2014

Re: K140407
Trade/Device Name: FilmArray Gastrointestinal (GI) Panel
Regulation Number: 21 CFR 866.3990
Regulation Name: Gastrointestinal microorganism multiplex nucleic acid-based assay
Regulatory Class: II
Product Code: PCH, OOI
Dated: February 13, 2014
Received: February 18, 2014

Dear Ms. Lingenfelter:

We have reviewed your Section 510(k) premarket notification of intent to market the device referenced above and have determined the device is substantially equivalent (for the indications for use stated in the enclosure) to legally marketed predicate devices marketed in interstate commerce prior to May 28, 1976, the enactment date of the Medical Device Amendments, or to devices that have been reclassified in accordance with the provisions of the Federal Food, Drug, and Cosmetic Act (Act) that do not require approval of a premarket approval application (PMA). You may, therefore, market the device, subject to the general controls provisions of the Act. The general controls provisions of the Act include requirements for annual registration, listing of devices, good manufacturing practice, labeling, and prohibitions against misbranding and adulteration. Please note: CDRH does not evaluate information related to contract liability warranties. We remind you, however, that device labeling must be truthful and not misleading.

If your device is classified (see above) into either class II (Special Controls) or class III (PMA), it may be subject to additional controls. Existing major regulations affecting your device can be found in the Code of Federal Regulations, Title 21, Parts 800 to 898. In addition, FDA may publish further announcements concerning your device in the Federal Register.

Please be advised that FDA's issuance of a substantial equivalence determination does not mean that FDA has made a determination that your device complies with other requirements of the Act or any Federal statutes and regulations administered by other Federal agencies. You must comply with all the Act's requirements, including, but not limited to: registration and listing (21 CFR Part 807); labeling (21 CFR Parts 801 and 809); medical device reporting (reporting of medical device-related adverse events) (21 CFR 803); good manufacturing practice requirements as set forth in the quality systems (QS) regulation (21 CFR Part 820); and if applicable, the electronic product radiation control provisions (Sections 531-542 of the Act); 21 CFR 1000-1050.

If you desire specific advice for your device on our labeling regulations (21 CFR Parts 801 and 809), please contact the Division of Industry and Consumer Education at its toll-free number (800) 638 2041 or (301) 796-7100 or at its Internet address http://www.fda.gov/MedicalDevices/ResourcesforYou/Industry/default.htm. Also, please note the regulation entitled, "Misbranding by reference to premarket notification" (21CFR Part 807.97). For questions regarding the reporting of adverse events under the MDR regulation (21 CFR Part 803), please go to http://www.fda.gov/MedicalDevices/Safety/ReportaProblem/default.htm for the CDRH's Office of Surveillance and Biometrics/Division of Postmarket Surveillance.

You may obtain other general information on your responsibilities under the Act from the Division of Industry and Consumer Education at its toll-free number (800) 638-2041 or (301) 796-7100 or at its Internet address http://www.fda.gov/MedicalDevices/ResourcesforYou/Industry/default.htm.

Sincerely yours,

John Hobson -S For

Sally Hojvat, M.Sc., Ph.D.
Director
Division of Microbiology Devices
Office of In Vitro Diagnostics
and Radiological Health
Center for Devices and Radiological Health

Enclosure

DEPARTMENT OF HEALTH AND HUMAN SERVICES
Food and Drug Administration

Indications for Use

Form Approved: OMB No. 0910-0120
Expiration Date: January 31, 2017
See PRA Statement on last page.

510(k) Number *(if known)*

K140407

Device Name

FilmArray Gastrointestinal (GI) Panel

Indications for Use *(Describe)*

Indications for Use

The FilmArray Gastrointestinal (GI) Panel is a qualitative multiplexed nucleic acid-based *in vitro* diagnostic test intended for use with the FilmArray instrument. The FilmArray GI Panel is capable of the simultaneous detection and identification of nucleic acids from multiple bacteria, viruses, and parasites directly from stool samples in Cary Blair transport media obtained from individuals with signs and/or symptoms of gastrointestinal infection. The following bacteria (including several diarrheagenic *E. coli/Shigella* pathotypes), parasites, and viruses are identified using the FilmArray GI Panel:

- *Campylobacter* (*C. jejuni/C. coli/C. upsaliensis*)
- *Clostridium difficile* (*C. difficile*) toxin A/B
- *Plesiomonas shigelloides*
- *Salmonella*
- *Vibrio* (*V. parahaemolyticus/V. vulnificus/V. cholerae*) including specific identification of *Vibrio cholerae*
- *Yersinia enterocolitica*
- Enteroaggregative *Escherichia coli* (EAEC)
- Enteropathogenic *Escherichia coli* (EPEC)
- Enterotoxigenic *Escherichia coli* (ETEC) *lt/st*
- Shiga-like toxin-producing *Escherichia coli* (STEC) *stx1/stx2* (including specific identification of the *E. coli* O157 serogroup within STEC)
- *Shigella*/Enteroinvasive *Escherichia coli* (EIEC)
- *Cryptosporidium*
- *Cyclospora cayetanensis*
- *Entamoeba histolytica*
- *Giardia lamblia* (also known as *G. intestinalis* and *G. duodenalis*)
- Adenovirus F 40/41
- Astrovirus
- Norovirus GI/GII
- Rotavirus A
- Sapovirus (Genogroups I, II, IV, and V)

The FilmArray GI Panel is indicated as an aid in the diagnosis of specific agents of gastrointestinal illness and results are meant to be used in conjunction with other clinical, laboratory, and epidemiological data. Positive results do not rule out co-infection with organisms not included in the FilmArray GI Panel. The agent detected may not be the definite cause of the disease.

Concomitant culture is necessary for organism recovery and further typing of bacterial agents.

This device is not intended to monitor or guide treatment for *C. difficile* infection.

Due to the small number of positive specimens collected for certain organisms during the prospective clinical study, performance characteristics for *E. coli* O157, *Plesiomonas shigelloides*, *Yersinia enterocolitica*, Astrovirus, and Rotavirus A were established primarily with retrospective clinical specimens.

Performance characteristics for *Entamoeba histolytica*, and *Vibrio (V. parahaemolyticus, V. vulnificus*, and *Vibrio cholerae)* were established primarily using contrived clinical specimens.

Negative FilmArray GI Panel results in the setting of clinical illness compatible with gastroenteritis may be due to infection by pathogens that are not detected by this test or non-infectious causes such as ulcerative colitis, irritable bowel syndrome, or Crohn's disease.

A gastrointestinal microorganism multiplex nucleic acid-based assay also aids in the detection and identification of acute gastroenteritis in the context of outbreaks.

Type of Use *(Select one or both, as applicable)*

☒ Prescription Use (Part 21 CFR 801 Subpart D) ☐ Over-The-Counter Use (21 CFR 801 Subpart C)

PLEASE DO NOT WRITE BELOW THIS LINE – CONTINUE ON A SEPARATE PAGE IF NEEDED.

FOR FDA USE ONLY

Concurrence of Center for Devices and Radiological Health (CDRH) *(Signature)*

John Hobson -S
2014.05.02 11:59:19 -04'00'

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